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Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
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STREET: 1840 Dehavilland Drive
CITY: Thousand oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER: USA
ZIP: 91230-1789
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
SUFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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US-08-133-688-22

US-08-793-624-47

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US-08-396-001-12

US-09-323-433A-12

US-09-323-433A-12

US-09-142-511A-4

US-08-872-979-3

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APPLICANT: BOYLe, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REFERENCE: A-45.BEV
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR PILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
NUMBER OF SEQ ID NOS: 40
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Best Local Simi
Matches 316;
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SEQ ID NO 2
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APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Manmalian Cell Surface Antigens; Related
TITLE OF INVENTION: Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
CLASSIFICATION: 56
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 56
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0686
                                                                                                                                                                                                                                                                                                 08-989-362-2
Sequence 2, Application US/08989362
Patent No. 6242586
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)4852-9196
TELEFA: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                            DQDATYFGAFKVQDID 316
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Best Local Simi
Matches 316;
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                   Sequence 11, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk Computer: Apple Power Macintosh OPERATING SYSTEM: Apple Operating System 7.5.5 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILLING DATE: 22 DECEMBER 1997
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPRAX: (206)233-0644
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100.0%; Pre
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity
Matches 217; Conserv
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US-08-996-139-11
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EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 219
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                                                                                                      APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.7%; Score 217; DB 4; Length 294; 100.0%; Pred. No. 6.7e-210; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Apple Fower Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                       3: Immunex Corporation, Law Department
51 University Street
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APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
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Sequence 11, Application US/08995659 Patent No. 6242213
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                   Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 0
FILING DATE: 07 MARCH 1997
                                      GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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LENGTH: 294 amino acid
TYPE: amino acid
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Best Local Similarity 100.
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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APPLICATE: INCREMENTATION: OSTEOPTOTEGERIN BINDING Proteins and Receptors TITLE OF INVENTION: OSTEOPTOTEGERIN BINDING Proteins and Receptors FILE REFERENCE: A-451Brv CURRENT APPLICATION NUMBER: US/09/052,521C CURRENT FILING DATE: 1998-03-30 PRIOR PLINGING DATE: 1997-06-23 PRIOR PLINGING DATE: 1997-06-23 PRIOR APPLICATION NUMBER: 08/842,842 PRIOR APPLICATION NUMBER: 08/842,842 NUMBER OF SEQ ID NOS: 40 SOUTH OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BOYLE, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
FILE REPERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide
US-09-052-521C-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Oligonucleotide
US-09-052-521C-34
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Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 27; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NAASIPSGSHKVTLSSWYHDRGWAKIS 27
                         Sequence 34, Application US/09052521C Patent No. 6316408 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 33, Application US/09052521C; Patent No. 6316408
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; Sequence 13, Application US/08996139
; Patent No. 6017729
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Best Local Similarity 100.(
Matches 22; Conservative
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US-09-052-521C-34
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LENGTH: 28
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LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 EAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 CFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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                                                                                                                                                                                                                                                         Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION CUNROWND
PRIOR APPLICATION TAIN
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: CUNROWND
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/72,330
FILING DATE: 3 DECEMBER 1996
ATONNEY/AGENT INFORMATION:
NAME: PEFKING PARTICIA ANNE
REFERRENCE/DOCKET NUMBER: 34,693
REFERRENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 FKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                             Sequence 11, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEO ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
                                                                                                                                                                                                      APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
                                                             US-09-215-649A-11
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
CORPATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILLING DATE: 17-Dec-1998
CLASSIFICATION: GUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.0%; Score 22; DB 4; Length 317;
100.0%; Pred. No. 4.3e-14;
ive 0; Mismatches 0; Indels
                                                                MEDIUM'TYE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: USSN 08/712,330
FILING DATE: 07 MARCH 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 33 DECEMBER 1996
CLASSIFICATION NUMBER: 34,693
REPERBENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
PROJESTRATION UNBER: 2852-A
TELECOMMUNICATION INFORMATION:
THE PRODUME: APPLICATION NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
THE PRODUMER: 10 TO THE PRODUMER: 2005-CA 10 TO TA 10 TO T
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TITLE OF INVENTION: Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 100.0%; Pred. No. 4.3
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 VNQDGFYYLYANICFRHHETSG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206)587-0430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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Patent No. 644213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Gallbert, Laurent
APPLICANT: Gallbert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
APPLICATION NUMBER: USSN 60/064,671
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPRAX: (206)587-0430
TELEPRAX: (206)587-0430
TELEPRAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 317 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             Seattle
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                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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Gaps

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CTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-09-052-521C-35
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100.0%; Pred. No. 2.8e-10;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08870518
Patent No. 592556
GENERAL INFORMATION:
APPLICANT: Balcheva-Gargova, Zoya
APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,518
FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
FILING DATE: 06-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION NUMBER: 32,983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8; DB 2;
Pred. No. 7;
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TELECOMMUNICATION: TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR PRIING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%; S
100.0%;
                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 459 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 VYVVKTSIKIPSSHNLM 255
                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.4%
Best Local Similarity 100.(
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VYVVKTSIKIPSSHNLM 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 459 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                   SEQ ID NO 35
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:

TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR FILING DATE: 1997-06-23
PRIOR FILING DATE: 1997-04-16
NUMBER: OF SEQ ID NOS: 40

2 ID NO 4

2 ID NO 4
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APPLICANT: Boyle, William J.
IIILE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 22; DB 4; Length 317;
100.0%; Pred. No. 4.3e-14;
Live 0; Mismatches 0; Indels
             FILING DATE: CURROWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: O' MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INCORMATION:
NAME: PERKINS, PARTICIA
REGISTRATION NUMBER: 34,693
REFERRENCE/DOCKET NUMBER: 2851-A
TELEPAN: (206)587-0430
TELEPAN: (206)587-0430
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
      APPLICATION NUMBER: 08/996,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/09052521C
Patent No. 6316408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09052521C Patent No. 6316408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%
Best Local Similarity 100.(
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human
US-09-052-521C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-052-521C-35
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Patent No. 590320,
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hyama, Jun
APPLICANT: Hyama, Jun
APPLICANT: Skinner, Margot
APPLICANT: Scinner, Margot
APPLICANT: Scint, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: U.S. Patent Application No. 5985287 08/873,970 June 12, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
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Patent No. 5985287
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janer
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEPAX: 206-269-0563
                          MEDIUM TYPE: DISNELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                      COMPUTER READABLE FORM:
                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-997-362-4
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US-08-997-080-4
Sequence 4, Application US/08997080
SECONTINE TAN APPLICANT: WARSON, JAMES D.
APPLICANT: TAN PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
CORRESPONDENCE: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
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    Gaps
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duery Match 2.5%; Score 8; DB 2 Best Local Similarity 100.0%; Pred. No. 62; Matches 8; Conservative 0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                         Sequence 2, Application US/08804227C Patent No. 5876991
GENERAL INFORMATION:
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-804-227C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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20 PAPAPPPA 27
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                                      37 PAPAPPPA 44
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Matches
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APPLICANT: Tan, Paul
APPLICANT: Tan, Paul
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Moss
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                 Length 21;
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100.0%; Pred. No. 3.7;
tive 0; Mismatches
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                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                              Query Match 2.2%; Score 7; DB 3
Best Local Similarity 100.0%; Pred. No. 3.7
Matches 7; Conservative 0; Mismatches
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REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/095,855
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
AUGUST OF THE STATE AUGUST OF THE S
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Sequence 4, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.2
Best Local Similarity 100.
Matches 7; Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-095-855-4
                                     single
                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
         TYPE: amino acid
STRANDEDNESS: sir
                                                                    linear
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STREET: ZOUL
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                 ; TOPOLOGY: li;
; MOLECULE TYPE:
US-08-873-970-4
                                                                                                                                                                                                                                                                                                                                            37 PAPAPPP 43
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 98121
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APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347 FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REPERENCE/DOCKET UNMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2%; Score 7; DB 2
100.0%; Pred. No. 3.7
ative 0; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08873970 Patent No. 6001361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ery Match
est Local Similarity 100.v.
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                                                                                                                                                                                                                                                 TELEFAX: 206-269-0563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
US-08-873-970-4
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Length 21;

DB 4;

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2.2%; Scc. 100.0%; Pred. No. 0; Mismatches
EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23 WUMBER OF SEQ ID NOS: 194 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BECH, Lene M.
APPLICANT: SORENSEN, Steen B.
APPLICANT: VAAG, Pla
                                                                                                                  TYPE: PRT
ORGANISM: Mycobacterium vaccae
US-09-324-542-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LADAS & PARRY STREET: 26 WEST 61 STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212) 708-18
(212) 246-8959
                                                                                                                                                                                                                           Query Match 2.28
Best Local Similarity 100.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 41 Amino Acids TYPE: Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 246-895
TELEX: 233288
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEW YORK
                                                                                                                                                                                                                                                                                                          37 PAPAPPP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cli.
STATE: N. 10023
                                                                                                                                                                                                                                                                                                                                                  2 PAPAPPP 8
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US-08-640-847C-3
                                                                             SEQ ID NO 4
LENGTH: 21
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                                                                                                                                                                                                                     APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Schner, Margot
APPLICANT: Schner, Margot
APPLICANT: Schner, Linda
TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
AUDMER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09324542
Patent NO. 6338978
GENERAL INFORMATION.
APPLICANT: Tan, Paul L.J.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
FILE REPERBERS: 1000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2%; Score 7; DB 4; Length 21; 100.0%; Pred. No. 3.7; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CHRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/705,347A FILING DATE: 28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 206.269.0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   Sequence 4, Application US/08705347A
Patent No. 6284255
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206.269.0563
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
37 PAPAPPP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 PAPAPPP 43
                                     2 PAPAPPP 8
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2 PAPAPPP 8
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                                                                                                                       US-08-705-347A-4
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Best Local Si
Matches 7,
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STATE:
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COUNTRY: 10023
COUNTRY: 10023
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4 Disk 1.44 MB
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,847C
FILING DATE: 26-UON-1996
CLASSIFICATION: 426
PRIOR APPLICATION UNMBER: PCT/DK94/00420
FILING DATE: 08-NOV-1994
APPLICATION NUMBER: DK001266/93
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,066
                                                                                                                                                                                                                                          APPLICANT: BREDDAM, Klaus
TILLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 41;
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Sequence 3, Application US/08640847C Patent No. 5993865
                                                                                                                                       APPLICANT: VAAG, Pla
APPLICANT: WILDBJERG, Marianne
APPLICANT: BERNFELDT, Thorkild
APPLICANT: LEAH, RObert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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RESULT 25
US-08-284-391B-35
US-08-284-391B-35
Squence 35, Application US/08284391B
Patent No. 5851828
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: TELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
STRPER"
                                                                        APPLICANT: LEAH, ROBERT
APPLICANT: BREDDAM, Klaus
TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT
NUMBER OF SEQUENCES: 41.
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
ZIP: 10023
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44 MB
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Wordperfect Windows for Workgroups 3.11
SOFTWARE: Wordperfect Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,847C
FILING DATE: 26-JUN-1996
CLASSIFICATION A426
PRIOR APPLICATION NUMBER: PCT/DK94/00420
FILING DATE: 08-NOV-1994
APPLICATION NUMBER: DK001266/93
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: U-010781-0
REGISTRATION NUMBER: U-010781-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%; Score 7; DB 2;
100.0%; Pred. No. 7.1;
tive 0; Mismatches
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CITY: Boston
SPATE: MA
COUNTRY: USA
                                        MULDBJERG, Marianne
BEENFELDT, Thorkild
    Steen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 233288
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 Amino Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 708-1890
TELEFAX: (212) 246-8959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.v
  SORENSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acids
TOPOLOGY: Linear
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                                                            APPLICANT:
APPLICANT:
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APPLICANT: SORENSEN, Steen B.
APPLICANT: SORENSEN, Pia
APPLICANT: WLDBJERG, Marianne
APPLICANT: BEENFELDT, Thorkild
APPLICANT: BEENFELDT, Thorkild
APPLICANT: BREDDAM, Klaus
APPLICANT: BREDDAM, Klaus
APPLICANT: BEEDENESS: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
STATE: NY
ZIP: 10023
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: 31.1/4" Disk 1.44 MB
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: Worderfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,847C
    Indels
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Pred. No. 7.1;
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Best Local Similarity 100.0%; Pred. No. ...
"**^hes 7; Conservative 0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPELICATION NUMBER: US/08/640,847C
FILING DATE: 26-JUN-1996
CLASSIFICATION: 426
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK94/00420
FILING DATE: 08-NOV-1994
APPLICATION NUMBER: DX001266/93
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MASS, CILIFORT J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
REFERENCE/DOCKET NUMBER: U-010781-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U-010781-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-640-847C-12; Sequence 12, Application US/08640847C; Patent No. 5993865; GENERAL INFORMATION:
                                                                                                                                                                      Sequence 9, Application US/08640847C Patent No. 5993865
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 708-1890
TELEFAX: (212) 246-8959
TELEEX: 233288
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 41 Amino Acids
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BECH, Lene M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino Acids
                                                                                                                                                                                                            GENERAL INFORMATION:
                                      170 NAASIPS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 NAASIPS 176
                                                            1111111
15 NAASIPS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-640-847C-9
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Matches
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0; Indels Length 41;

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Length 58;
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ADDION TYPE: E10Ppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,498
FILING APPLICATION BOTA:
PRINCE APPLICATION NUMBER: PCT/GB94/01636
FILING APPLICATION DATA:
APPLICATION NUMBER: BCT/GB94/01636
FILING APPLICATION DATA:
APPLICATION NUMBER: GB 9317816.8
FILING DATE: 29-JUL-1994
PRIOR APPLICATION NUMBER: GB 9317816.8
FILING DATE: 27-AUG-1993
PRIOR APPLICATION NUMBER: GB 9316158.6
FILING DATE: GB 9316158.6
FILING DATE: 04-AUG-1993
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 4; Pred. No. 9.90; Mismatches
                                                                                                                                                                                                                     00786/247001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 New York Avenue, N.W. CITY: Washington
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-591-498-10; Sequence 10, Application US/08591498; Patent No. 5773694
                                                                                                                                                                        NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/CDCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 58 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-218-950-35
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COUNTRY:
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APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
CORRESPONDENCE: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                MELLALING DATE: 18M COMPALALING DERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: 1994
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score ,,
100.0%; Pred. No. 9.9
                                                                                                                                              FILING DATE: 02-AUG-1974 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/65,961
FILING DATE: 07-MAR-1991
ATTORNEY/ARENT INFORMATION:
NAME: Elbing/Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
TELEFANONE: 617-428-0200
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APPLICATION NUMBER: US/08/284,391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Clark & Elbing LLP STREET: 176 Federal Street
    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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LENGTH: 58 amino acids
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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ADDRESSEE: Department of Biotechnical Sciences, Agricultural
ADDRESSEE: University of No. 6031152way and Agricultural Biotechnology
ADDRESSEE: Program NRC
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AUTHORS: Olsen, Odd-Arne
TITLE: Promoter of a Liplid Transfer Protein Gene
TITLE: Expressed in Barley Aleurone Cells Contains
TITLE: Similar myb and myc Recognition Sites as the Maize
TITLE: Bz-McC Allele
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100.0%; Pred. No. 19;
vative 0; Mismatches
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Olsen, Odd-Arne
APPLICANT: Alla, Roger
APPLICANT: Linnestad, Casper
TITLE OF INVENTION: Promoter from a Lipid
TITLE OF INVENTION: Transfer Protein Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5
COMBUTER: IBM COMBUTER: IBM COMBUTER: IBM COPERATING SYSTEM: WINDOWS 98
SOFTWARE: WORD PROCESSING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,609A
FILING DATE: 20-NOV-1996
CLASSIFICATION NUMBER: PCT\N095\00042
FILING DATE: 3.02.95
APPLICATION NUMBER: PCT\N095\00042
FILING DATE: 3.02.95
ATTORNEY AGENT INFORMATION:
NAME: Thaddius J. Carvis
REGISTRATION NUMBER: 833-P0016A
FELEFAN: 203-327-1096
INFORMATION FOR SEQ ID NO: 4:
FELEFAN: 203-327-1096
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 residues
TYPE: and a caid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE:
ORIGINAL SOURCE:
CREANING BAILEY
PUBLICATION INFORMATION:
ANTHORS:
ORIGINAL BAILEY
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: No. 6031152way
ZIP: N-1432
COMPUTER FRADABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                        Sequence 4, Application US/08702609A Patent No. 6031152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Lonneborg, Anders
: Kalla, Roger
: Olsen, Odd-Arne
Promoter of a Lipid Ti
Expressed in Barley A.
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Best Local Similarity 100..
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                     67 NAASIPS 73
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AUTHORS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPAINED
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,498
FILING DATE: 25-JAN-1996
CLASSIFICATION NUMBER: PCT/GB94/01636
FILING DATE: 29-JUL-1994
PRIOR APPLICATION NUMBER: GB 9317816.8
FILING DATE: 27-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9316158.6
FILING DATE: 104-AUG-1993
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 anning acids
TVAPE: ATABACTERISTICS:
LENGTH: 93 anning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMAN DARBY & CUSHMAN
ADDRESSEE: Intellectual Property Group of
ADDRESSEE: PILLSBURY MADISON & SUTRO LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
TITLE OF INVENTON: ANTIMICROBIAL PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 7; DB 1, 100.0%; Pred. No. 15; tive 0; Mismatches
                                                                                                                                                                                                           2.2%; Score 7; DB 1
100.0%; Pred. No. 15;
Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  ULT 28
08-591-498-14
Equence 14, Application US/08591498
Patent No. 5773694
Patent no. 5773694
                   ; TYPE: amino acid
; STRANDEDRES: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORIGINAL SOURCE:
; ORGANISM: PAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.2
Best Local Similarity 100.
Matches 7; Conservative
93 amino acids
                                                                                                                                                                                                        Query Match · 2.2
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Zm-nsLTP
US-08-591-498-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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LENGTH:
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                                                                            GENERAL INFORMATION:
APPLICANT: Michael E. Selsted
TITLE OF INVENTION: Antimicrobial Peptides and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,149C
FILING DATE: 14-February-1997
PRIOR APPLICATION NUMBER: 60/011,834
FILING DATE: 16-February-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,34
FREISTRATION NUMBER: 38,34
FREISTRATION NUMBER: 38,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.2%; Score 7; DB 3; Best Local Similarity 100.0%; Pred. No. 31; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 07306/009001
TELECOMMUNICATION INFORMATION:
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Sequence 211, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ausubel, Frederick
Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
                                         Sequence 3, Application US/08799149C Patent No. 6008195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
LOCATION: 39..598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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|13 LALLGLG 19
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ZIP: 92037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-799-149C-3
                   JS-08-799-149C-3
                                                                                                                                                                                                                                                                               STATE:
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AUTHORS: Mundy, John
TITLE: Structure and Expression of the Barley Lipid Transfer Protein Promoter
JOURNAL: Plant Molecular Biology
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                                                                                                                                                                                                                                                                                                     Plant Molecular Biology Laboratory,
Department of Biotechnical Sciences, Agricultural
University of No. 6031152way and Agricultural Biotechnology
Program NRC
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100.0%; Pred. No. 19;
iive 0; Mismatches
                                                                                                                                                                  APPLICANT: Olsen, Odd-Arne
APPLICANT: Kalla, Roger
APPLICANT: Linnestad, Casper
TITLE OF INVENTION: Promoter from a Lipid
TITLE OF INVENTION: Transfer Protein Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,609A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRICA PAPLICATION DATA:
APPLICATION NUMBER: PCT\N095\00042
FILING DATE: 23.02.95
ATTORNEY AGENT INFORMATION:
NAME: Thaddius J. Carvis
REGISTRATION NUMBER: 26110
TREFERENCE/DOCKET NUMBER: 36120
TRECECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                      Sequence 6, Application US/08702609A Patent No. 6031152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Skriver, Karen
AUTHORS: Leah, Robert
AUTHORS: Muller-Uri, Frieder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: WINDOWS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: 203-32/ LOS INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS: LENGTH: 117 residues TYPE: amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: No. 6031152way
ZIP: N-1432
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                                                                                                                                               GENERAL INFORMATION:
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DATE: 16.09.91
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ADDRESSEE:
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MOLECULE TYPE: protein
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Sequence 47, Application US/08420235B

Patent No. 5801042

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09171461

Patent No. 6335016

GENERAL INFORMATION:

APPLICANT: Cotten, Matthew

TILLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus

FILE REFERENCE: 0652.180000

CURRENT APPLICATION NUMBER: US/09/171,461

CURRENT FILING DATE: 1999-01-12

EARLIER APPLICATION NUMBER: PCT/EP97/01944

EARLIER FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 5-4

SOFFWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 36;
tive 0; Mismatches
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 211
LENGTH: 207
                                                                                                                           ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-211
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ORGANISM: CELO Virus
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89 APSAPAP 95
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09-171-461-11
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LENGTH: 223
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Patent No. 5830759
GENERAL INFORMATION:
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma TITLE OF INVENTION: Virus Sequences And Uses Thereof NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2%; Score 7; DB 1;
100.0%; Pred. No. 47;
ative 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,235B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 514
ATTOREY/AGENT INFORMATION:
NAME: White ESQ., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45,185-A
TELEPHONE: 212-278-040
TELEPHONE: 212-391-0526
INFORMATION POSSED ID NO: 22:
                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.2
Best Local Similarity 100.
Matches 7; Conservative
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LENGTH: 301 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-420-235B-47
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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US-08-343-101A-22
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; 0; Gaps Query Match 2.2%; Score 7; DB 2; Length 301; Best Local Similarity 100.0%; Pred. No. 47; Matches 7; Conservative 0; Mismatches 0; Indels

55 GLGLGQV 61 ||||||| 42 GLGLGQV 48 δλ

qq

Search completed: July 15, 2002, 11:06:45 Job time: 135 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 15, 2002, 11:06:51; Search time 13.45 Seconds (without alignments) 909.694 Million cell updates/sec Run on:

US-09-671-658A-2 316 1 MRRASRDYGKYLRSSEEMGS......LLDPDQDATYFGAFKVQDID 316

Title: Perfect score: Sequence:

105224 seqs, 38719550 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

Scoring table:

l size :

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	m tumor ne	O14788 h tumor nec	P79148 canis famil	Q96rd6 homo sapien	3 ношо	homod	homo	papio	Q9tst4 felis silve		Q9pgu4 xylella fas			petrom	Q42976 oryza sativ	P23096 oryza sativ	horder			m		Q07178 rhodobacter	Q9ubm1 homo sapien	P06892 xenopus lae	Q64757 avian adeno	P09564 homo sapien		3 ношо	рошо	snw	_	epstein-	P31259 gallus gall
SUMMARIES	ID	TN11_MOUSE	TN11_HUMAN	B1AR_CANFA	PAN2_HUMAN	HES2_HUMAN	MLEV_HUMAN	GPBB_HUMAN	GPBB_PAPCY	B3AR_FELCA		- 1			NULM_PETMA	NLT4_ORYSA	NLT1_ORYSA	NLT1_HORVU	NLT3_ORYSA	NLT1_SORBI	NLT2_ORYSA	NLTP_MAIZE *	NIU1_RHOCA	PEMT_HUMAN	H1A_XENLA	PIV6_ADEG1	CD7_HUMAN	TRIC_XENLA	HXB4_HUMAN	- 1	CDX1_MOUSE	1	- 1	HXB1_CHICK
	Length DB						194 1				29	1193 1		91 1	96 1	99 1	116 1	117 1	117 1	118 1	118 1	120 1	135 1	198 1	209 1	223 1	240 1	243 1	251 1			272 1		309 1
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P03342 avian splee P46955 saccharomyc	P74438 synechocyst O58820 methanococc	002755 bos taurus P17327 salmonella	015011 homo sapien P49137 homo sapien	_	002662 canis famil	Q16186 homo sapien	Q9jkv1 mus musculu	Q9jmb5 rattus norv	P47040 saccharomyc	Q90678 g platelet-	Q9hev5 neurospora	Q9z0z7 mus musculu
GAG_AVISN NCA3_YEAST	PYRC_SYNY3 COMC_METJA	CEBB_BOVIN PROW_SALTY	HERP_HUMAN	ODP2_MYCPN	B3AR_CANFA	G110_HUMAN	G110_MOUSE	G110_RAT	BTN1_YEAST	PAFA_CHICK	ASD4_NEUCR	KLF5_MOUSE
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ALIGNMENTS

CINGUIDING	30L		I to CCT-2001 (Rel. 40, Last annotation update)			Mus musculus (Mouse).				TISSU		Kalac	"TRANCE is a novel ligand of the tumor				-			Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y	A Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,		T differentiation and activation.";	[3]		C TISSUE=Bone marrow stroma;		Mochizuki SI., Tomoyasu A., Yano K., Goto M., Murakami	Morinaga T., Higashio K., Udagawa N., Takanashi N., Suda "Osteoclast differentiation factor is a ligand for			[4] N
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: DEFICIENCY IN THEFT11 RESULTS IN FAILURE TO FORM LOBULD-ALVEOLAR AMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE GOTSOPDETNOSIS, WITH PROCINCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA, WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN HYPERTROPHIC CHONDROCYTES.
                                                                                                                                                                                                                                           -1-FUNCTION: OSTEOCIAST DIFFERENTIATION AND ACTIVATION FACTOR.

AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS
BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE
REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.
-1-SUBCELLULAR LOCATION: Type II membrane protein (Potential).
-1-TISSUE SPECTRICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT
NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS
BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE
TRABECULAR BONE AND LUNG.
                                                                                                           "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
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R EMBL; AF013170; AAC71061.1; -.

R EMBL; AB008426; BAA25425.1; -.

R EMBL; AB003426; BAA37259.1; -.

R EMBL; AB036798; BAA97259.1; -.

R EMBL; AB036798; DAR97259.1; -.

R EMBL; AB036798; TNF_5.1.

R InterPro; IPR003478; TNF_5.1.

Prodom; PR008600; TNF_5; 1.

PROSITE; PS00251; TNF_1; FALSE_NEG.

R PROSITE; PS50049; TNF_2; 1.

R Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
               TISSUE-Thymic lymphoma;
MEDILINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                               Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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08DF63A2BE00967A CRC64;
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262 2
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316 AA;
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                                                                                             Galibert L.;
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TRANSMEM
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CARBOHYD
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TW11_HUMAN STANDARD, PRT; 317 AA.
014788; 014723; 09P203;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."; J. Biol. Chem. 272:25190-25194(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                   VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
                                                                          AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
                                                                                                             AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
                                                                                                                                                                                                                          VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lymph node;
MEDLINE=98227661; PubMed=9568710;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                               241 VVKTSIKIPSSHNLMKGGSTKNMSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP
                                                                                                                                                    VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Bone marrow, and Peripheral blood;
MEDLINE-98032977; PubMed-9367155;
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation factor) (ODF).
TNFSF11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Thymocytes; MEDLINE-97460112; PubMed-9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2)
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                                                                                                                                                                                                                                                                                                                         301 DQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                    301 DQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                 TN11_HUMAN
                                     61
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61
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Gaps

; 0

0; Indels

0; Mismatches

Matches 316; Conservative

Query Match Best Local Similarity

100.0%; Score 316; DB 1; Length 316; 100.0%; Pred. No. 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                       formation.";
Biochast Commun. 269:532-536(2000).
Biocham. Biophys. Res. Commun. 269:532-536(2000).
-! FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AUGMENTS ABILITY OF DENDRITIC CELLS TO STINULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS. AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL HYPERCALCIARIA OF MALIGNANCY.
-!- SUPERCALCIARIA OF MALIGNANCY.
                                                                                                                                                                                                                                                              SECRETED (ISOFORM 2).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART, PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

-!- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.

-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
CYtokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                   Wagai M., Kyakumoto S., Sato N.; "Cancer cells responsible for humoral hypercalcemia express mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM 2).
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                                                           encoding a secreted form of ODF/TRANCE that induces osteoclast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 1; Length 317;
Pred. No. 1.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766176446348097F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT, 473 AA. P79148; 01-NOV-1997 (Rel. 35, Created) (NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) Beta-1 adrenergic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
MEDLINE=20175237; PubMed=10708588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD008600; TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 VNQDGFYYLYANICFRHHETSG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 VNQDGFYYLYANICFRHHETSG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF019047; AAB86811.1; -.
EMBL, AF053712; AAC39731.1; -.
EMBL, AF013171; AAC51762.1; -.
EMBL, AB037599; BAA90488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35478 MW;
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194
317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches .22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
171
198
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CARBOHYD
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                 APPROXIMATIVELY EQUAL AFFINITY.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
                                                                                                                                                         receptors.";
J. Recept. Signal Transduct. Res. 17:599-607(1997).
-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                            SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY CAPK) (POTENTIAL).
                            Euteleostomi;
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0
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                                                                                                             Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascieri M.A.,
Fong T.M.;
                                                                                                                               Fong T.M.; "Molecular cloning of the dog beta 1 and beta 2 adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family, Phosphorylation, Lipoprotein, Palmitate. DOMAIN (POTENTIAL).
         Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRIMTS; PR00237; GPCRHDDOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITATE (BY SIMILARITY). 361357F7DF9DBD7E CRC64;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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100.0%; Pre
0; '
                                                                                   SEQUENCE FROM N.A. MEDLINE=97364078; PubMed=9220370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50060 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U73207; AAB93648.1; -. HSSP; P07700; 1DEP.
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Best Local Similarity
Matches 9; Conserv
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278 APAPAPPA 286
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                                                         NCBI_TaxID=9615;
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TRANSMEM
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TRANSMEM
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LIPID
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δλ
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RESULT

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RADIDEMCE FROM N.A.

SEQUENCE FROM N.A.

MEDILISA-20057165; Pubmed-10591208;

RADINAMI I., HUNT A.R., COLLINS J.E., Bruskiewich R., Beare D.M.,

Clamp M., Sanhut A.R., Ainscough R., Burgess J.P. Babbage A.,

RADINAMI I., HUNT A.R., COLLINE S.E., CORNOT R.E., CORNOT B. Clark G., Clegs S.M.,

CORLEO V., COLLIGE R.E., CORNOT R.E., CORNOT R.D. DOCKTEE C.,

Burdery S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burdery D., Corby N.,

COVILLE G.J., COX A.V., Davis J., Davis D., Dockree C.,

RADINAMI R., T., Durbin R.M., Ellington A.E., Evans K.L., Fey J.M.,

RADINAMI R., French L., Garner A.A., Gilbert J.G.R., Govard M.E.,

RADINAMI R., French L., Garner A.A., Gilbert J.G.R., Govard M.E.,

RADINAMI R., Franch L., Garner A.M., Gilbert J.G.R., Govard M.E.,

RADINAMI R., Franch L., Garner A.M., Gilbert J.G.R., Govard M.E.,

RADINAMI R., Franch L., Garner A.M., Gilbert J.G.R., Govard M.E.,

RADINAMI R., Martyn I.D., Mashegoni-Wohammadi M.,

Matthe S.A., Mortimore B.J., Odeal C.N., Pavitt R., Pearson D., Philliance B.J., Odeal C.N., Pavitt R., Stuce C.D.,

RADINAMI R., Soott C.E., Speran C.A.,

RADING S.A., Mortimore B.J., Odeal C.N., Pavitt R., Stuce C.D.,

RADING S.A., Wortlind A., Hilliams E., Williamson H.,

Minteley M.N., Willey D., Williams L., Williams D., Williams S., Williamson H.,

Mitteley M.N., Willey D., Williams L., Williams S., Williams S.,

RADING S., Rogers J., Shindau M., Waldin M., Wall M.

RADING S., Rogers J., Shindau M., Wallin M., Walli S., P., Loh P., Malais E.,

RADING S., Rogers J., Shindau M., Walli M., Wallis J., Williams S., Willey D., Williams S., Murray J., Willey D., Williams S., Murray J., Willey D., Williams S.,

RADING S., Rogers J., Shindau M., Wandi S., Rowasaki K., Sasaki T.,

ROD T., Dorman A., Fang P., Fu Y., Hu P., Hu A., Kend D., Song L., Bann M., Shan S., Lai H., Yao Z., Zhan M., Vand S., Lin S., Willey D., Walley C., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                    Baranova A., Ivanov D., Skoblov M., Pestova A., Kelmanson I., Shagin D., Osman N., Lukyanov S., Panchin Y.; Mammalian pannexin family homologous to invertebrate gap-junction proteins are differentially expressed in nervous tissue."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: STRUCTURAL COMPONENT OF THE GAP JUNCTIONS.
-i- SUBSCELLULAR LOCATION: Integral membrane protein (Potential).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-i- SIMILARITY: BELONGS TO THE INNEXIN FAMILY.
                                         096RD6; 096RD5; 09UGX8; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:489-495(1999).
                         STANDARD;
                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                   Pannexin 2.
                         PAN2_HUMAN
                                                                                                                                                          PANX2
PAN2_HUMAN
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the Swiss Institute of Bioinformatics and the EMBL outstation

between the Swiss institute.

There are no restrictions on

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RATHER THAN THE CANONICAL E-BOX (CANNTG).

-!- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUGHO, A TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY HAIRY-RELATED PROTEINS (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE BASIC HELIX LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
PROTEIN FOR THEIR TRANSCRIPTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HES2_HUMAN STANDARD; PRT; 173 AA.
09Y543; 09Y542;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription factor HES-2 (Hairy and enhancer of split 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                   Length 633;
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                             MISSING (IN ISOFORM 2).
C89CF833E0251D58 CRC64;
                                                                                                                                                  Alternative splicing.
                                                                                                                                                                                                                                                                                                                 2.8%; Score 9; DB 1;
100.0%; Pred. No. 0.45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                            POTENTIAL
                                                                                           EMBL; AF398510; AAK91715.1; -. EMBL; AF398511; AAK91716.1; -. EMBL; AL022328; CAB63042.1; -.
                                                                                                                                                                                                                                                              69478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL031848; CAB46198.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL031848; CAB46199.1; -
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InterPro; IPR001092; HLH_dim.
InterPro; IPR003650; Orange.
                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                         Conservative
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SMART; SM00353; HLH; 1.
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136
239
305
124
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                                                                                                                                                                                                                                                            633 AA;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             486 APAPAPPPA 494
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                                                                                                                                                                                                                                                                                                                                                                                           36 APAPAPPPA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                   junction;
                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                            TRANSMEM
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Searched:

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Sequence:

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Run on:

Scoring table:

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1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRSMFLALLGLGLGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08842842
Patent No. 5843678
CENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE: ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/842,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1675; DB 2;
100.0%; Pred. No. 2.9e-157;
iive 0; Mismatches 0;
                US-08-339-214-32
US-08-815-140-32
US-09-815-140-25
US-09-290-640-25
US-09-39-214-8
US-08-339-214-8
US-08-339-214-30
US-08-360-362-2
US-08-184-422-8
US-08-184-422-8
US-08-44-922-4
US-08-446-923-4
US-08-446-923-4
US-08-446-923-4
US-08-446-923-4
US-08-446-923-4
US-08-441-055-4
US-08-449-189-12
US-08-449-189-12
US-08-449-189-12
US-08-449-189-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
  TOPOLOGY:
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  (without alignments)
588.299 Million cell updates/sec
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3, Appli
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                                                                                                                                                                                                                                                                1 MRRASRDYGKYLRSSEEMGS..........LLDPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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                                                                                                                                        July 15, 2002, 11:01:05; Search time 13.12 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/fB_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                                     Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-052-521C-2
US-08-096-139-11
US-08-996-139-11
US-09-215-649A-11
US-08-996-139-13
US-08-996-139-13
US-09-052-521C-4
US-09-052-521C-4
US-08-670-354-2
US-08-708-708-10
US-08-708-708-10
US-08-320-426-10
US-08-320-426-10
US-09-320-436-10
US-09-320-436-10
US-09-320-436-2
US-09-33-533A-6
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                     GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                        US-09-671-658A-2
1675
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Match I
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61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLODSTLESEDTLPDSCRRMKO 120

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Sequence 1 Sequence 7 Sequence 8

US-09-320-424-13 US-09-320-424-11 US-09-105-343A-7

240 236 229.5 224 183

US-09-320-424-6

Result Š Sequence Sequence

US-08-339-214-26 US-08-339-214-16

121 AFQGAVQKELOHIVGPORFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180

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VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRRASKDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPPAASRSMFLALLGLGLGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BOYLE, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE REFERENCE: A-451Brv
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 08/880,855
PRIOR PLICATION NUMBER: 08/842,842
PRIOR FILING DATE: 1997-04-16
                                                                                181 VTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
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100.0%; Pred. No. 2.9e-157;
ive 0; Mismatches 0;
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; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 DQDATYFGAFKVQDID 316
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Best Local Similarity 100.0
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-052-521C-2
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LENGTH: 316
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                                                                                                                                                        VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08989362
Patent No. 6242586
ENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine D.
TITLE OF INVENTION: Mammalian Cell Surface Antigens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,846
FILING DATE: 13-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, EGWin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX686
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/989,362
FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 316 amino acids
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       DQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-989-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 901 Califor
CITY: Palo Alto
STATE: California
COUNTRY: USA
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Sequence 11, Application US/08995659 Patent No. 6242213
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                                                                                                                                                                                                                          STATE: W. COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
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                                                                                                                                                                                  COUNTAL.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,139

FILING DATE: 22 DECEMBER 1997
                                APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                              3: Immunex Corporation, Law Department
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1554; DB 3;
Pred. No. 2.3e-145;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: O'T MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTONNEY/AGENT INFORMATION:
NAME: PERKINS, PARTICIA Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2851-A TELECOMMUNICATION INFORMATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
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LENGTH: 294 amino acids
TYPE: amino acid
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Pest Local Similarity 99.7
tches 293; Conservative
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                                                                                                                               STREET: 51 Univ
CITY: Seattle
STATE: WA
                                                                                                                ADDRESSEE:
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61 DSTHCFYRILRLHENADLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA, 120
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GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                     ADDRESSEE: Immunex Corporation, Law Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.8%; Score 1554; DB 4;
99.7%; Pred. No. 2.3e-145;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: USSN 08/712,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852
TELECOMMUNICATION: TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
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amino acid
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Matches 293; Conservative
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PRIOR APPLICATION DATA:
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RESULT 5 US-08-995-659-11

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WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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Matches 268; Conserv
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                                                                                                                                                                                                                                                                                                                STATE: WA
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                      US-08-996-139-13
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                   263
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241 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 294;
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
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                                                                                                                                                                              Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1554; DB 4;
Pred. No. 2.3e-145;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/ACENT INFORMATION:
NAME: PERKINS, PATLICIA Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11
                                                                                                  Sequence 11, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 294 amino acids
                                                                                                                                                                         Laurent
                                                                                                                                                     APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.8%;
99.7%;
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                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity 99.7%
Matches 293; Conservative
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                                                                                                                                                                       Galibert,
                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                  US-09-215-649A-11
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61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGG 59
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241 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
OPERATING SYSTEM: Apple Operating System 7.5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Receptor Activator of NF kappab NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
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84.3%; Pred. No. 7.4e
:ive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/996,139
22 DECEMBER 1997
                                                                                                                                                            Sequence 13, Application US/08996139 Patent No. 6017729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 317 amino acids
amino acid
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1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLH-APPPPAPHQPPAASRSMFVALLGLGLGQ 59
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239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
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APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY.

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,659
TITNG DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Immunex Corporation, Law Department 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.6%; Score 1417.5; DB 4;
84.3%; Pred. No. 7.4e-132;
11ve 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
CLASSIFICATION:
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08995659 Patent No. 6242213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 01
FILING DATE: 07 MARCH 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                   299 DPDQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 317 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-995-659-13
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Best Local Similarity
Matches 268; Conserva
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1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ 60

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60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                  61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                    KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                         HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
                                                                                                                                                                                                                                                                                                              239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
CORRATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
CLASSIFICATION: CUNKNOWND
PRIOR APPLICATION: CANKNOWND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappab
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/996,139
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USN 08/772,330
FILING DATE: 23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09215649A Patent No. 6271349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 317 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   299 DPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Brigham-Burke
APPLICANT: Peter R. Young
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
FILE REFERENCE: GH-50030
CURRENT APPLICATION NUMBER: US/09/072,993C
CURRENT PILLING DATE: 1998-05-06
PRIOR FILLING DATE: 1997-08-13
PRIOR FILLING DATE: 1997-08-13
PRIOR FILLING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/055,550
PRIOR APPLICATION NUMBER: 60/057,550
PRIOR FILLING DATE: 1997-08-29
SOFTWARE: FASELSEQ for Windows Version 3.0
240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ELQHIVGPQRFSGAPAMM 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 EGSWLDVAQRGKPEAQPFAHLT ----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 -----VRERGPQRVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steven R. Wiley and APPLICANT: Steven G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSE: Rathryn A. Anderson, Immunex Corporatic STRET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.4%; Score 258.5; DB 4; 26.4%; Pred. No. 1.3e-17; tive 54; Mismatches 113;
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; Patent No. 576323; GENERAL INFORMATION:
                                                        Query Match 15.4%
Best Local Similarity 26.4%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                          US-09-072-993C-3
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                                                                                                                                                                          60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRI 119
                                                                                                                                                                                                                                119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
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                                        Gaps
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                                                                                                  1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAPAASRSMFLALLGLGLGCG 60
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APPLICANT: BOYLE, William J.
TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors FILE OF INVENTION: US/09/052,521C
CURRENT APPLICATION NUMBER: US/09/052,521C
CURRENT FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
                                                                            1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ
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                                      31; Indels
DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.6%; Score 1417.5; DB 4;
84.3%; Pred. No. 7.4e-132;
11ve 16; Mismatches 31;
Score 1417.5; DB 4
Pred. No. 7.4e-132;
                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09052521C Patent No. 6316408
84.6%;
84.3%;
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Best Local Similarity 84.38
Matches 268; Conservative
                                      Matches 268; Conservative
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
PRGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-052-521C-4
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
                                                                                                                                                                                                                                                                                    43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                                                                                                                                                                                   10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64
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65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
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Patent No. 6046048
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                      Length 281;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                      54; Mismatches 113;
                                                                                                                                                                                                                   Pred. No. 1.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      15.4%; Score 258.5; 26.4%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                          101 QDSTLESEDTLPDSCRRMKQAFQGAVQK-----
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CURREWA APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
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NAME: Marschang, Diane L
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 281 amino acids
Amino Acid
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
                                                                                                                                                                                                                                      Conservative
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US-08-780-496-1
                                                                                                                                                                                                              Best_Local Similarity
Matches 78; Conserv
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                                                                                             ORGANISM: HOMO
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                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL----- 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY 64
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                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.4%; Score 258.5; ilarity 26.4%; Pred. No. 1.4e Conservative 54; Mismatches
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Sequence 1, Application US/08584031A

Sequence 1, Application US/08584031A

GENERAL NO. 6030945

GENERAL INCRAFION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: APO-2 LIGAND

FILE REFRENCE: 11669.22US03

CURRENT APPLICATION UNDEER: US/08/584,031A

UMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                            PLOGASTILLATION ....
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                   COMPUTER READABLE FORM:
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Best Local Similarity
Matches 78; Conserva
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                                                                                                                                                                         101 QDSTLESEDTLPDSCRRMKQAFQGAVQK------ELQHIVGPQRFSGAPAMM 146
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                                                                                                                                                                                                                                                                         224
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                                                           Gaps
                                                                                                                       10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64
                                                                                                                                                                                                                                                                                                                               NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMK
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                                                         51;
                   Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE THE FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                         Indels
                 15.4%; Score 258.5; DB 3; 26.4%; Pred. No. 1.4e-17; tive 54; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: G0064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6134.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: POTembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: No. 6171787e
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                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 847-938-2623
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PRIOR APPLICATION DATA:
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Query Match
Best Local Similarity
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Score 258.5; DB 4; Length 281; Pred. No. 1:4e-17;

15.4%; 26.4%;

Query Match Best Local Similarity

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10;
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                                                                                                               --ELQHIVGPQRFSGAPAMM 146
                                                                                                                                                                                       147 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                 197 NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
                                                                                                                                                                                                                                                                                     43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
 Gaps
                                                            10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF-----LKEDDSY 64
                                                                                                                                        225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                         257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
 51;
 Indels
 Mismatches 113;
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Search completed: July 15, 2002, 11:01:27 Job time: 22 sec

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July 15, 2002, 11:01:05; Search time 30.12 Seconds (without alignments) 1165.316 Million cell updates/sec US-09-671-658A-2 1675 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

al number of hits satisfying chosen parameters: 747574 segs, 111073796 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A_Geneseq_032802:* Database

1. /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:*
2. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3. /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
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122. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
123. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*
124. /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Human osteoprotege	Osteoclastogenesis	Amino acid sequenc	Murine TRANCE, Mu	Mouse OBM protein	Amino acid sequenc	Amino acid sequenc	Rat osteoclast dif	NF-kB receptor act	NF-kB receptor act	Murine receptor ac
		ID	AAW83194	AAW83017	AAW59654	AAY17874	AAY91024	AAY84418	AAY84419	AAB82092	AAW69956	AAW68292	AAE08737
			19	19	19	20	21	21	21	22	19	19	22
		Match Length DB	,	,		316				•			•
dР	Query	Match	1675 ~ 100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.3	92.8	92.8	92.8
		Score	1675	1675	1675	1675	1675	1675	1675	1597	1554	1554	1554
	Result	No.	Н	7	m	4	Ŋ	9	7	80	6	10	11

WPI; 1998-594578/50. N-PSDB; AAV70284.

(AMGE-) AMGEN INC.

Boyle WJ;

Mirine recentor ac	RANKI, (re	Human osteoprotege	NF-kB receptor act	NF-kB receptor act	Amino acid sequenc	Human receptor act	Human receptor act	Human full-length	Osteoclastogenesis	Amino acid sequenc	A murine OCIF-bind	Osteoclastogenesis	Human TRANCE. Hom	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	A murine osteoprot	Mouse FLAG-murine	An osteoprotegerin	An osteoprotegerin	DNA encoding osteo	Amino acid sequenc	Mouse OBM protein	Human RANKL. Homo	An osteoprotegerin	Mouse OBM protein	Mouse OBM protein	Human Apo-2 ligand	~	U	Tumour necrosis fa	Human Apoptosis in	Human apoptosis in
AAFOAA25	AAE01992	AAW83195	AAW69957	AAW68293	AAY84417	AAE08738	AAE04426	AAE01993	AAW83018	AAB84420	AAW83019	AAW83020	AAY17873	AAB08272	AAY84421	AAY84420	AAÝ84422	AAU08386	AAY84423	AAY84424	AAY84425	AAB08273	AAY91023	AAB67248	AAY84426	AAY91020	AAY91021	AAY27016	AAY27017	AAW76332	AAW95032	AAW27134	AAW19787
22	22	19	19	19	21	22	22	22	19	22	13	19	20	21	21	21	21	22	21	21	21	21	21	22	21	21	21	20	20	13	20	18	.18
294	294	317	317	317	317	317	317	317	317	501	244	246	245	160	173	187	173	170	188	182	173	160	139	152	173	74	24	281	281	279	279	281	281
9 69	92.8	84.6		84.6	•	•	84.6	84.6	84.1	78.7	77.4	66.1	65.7	51.0	50.9	50.9	50.3	49.6	48.0	47.4	46.0	45.9	44.5	44.2	43.7	23.1	17.0	15.5	15.5	15.4	15.4	15.4	15.4
1554	1554	1417.5	1417,5		1417:5		1417.5	1417.5	1409.5	1318	1297	1107	1101	855	852	852	842	830	804.5	794.5	771	768	746	741	732	387	285	259.5	259.5	258.5	258.5	258.5	258.5
12	3 1	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Human osteoprotegerin binding protein from the 32D-F3 ins. AAW83194 standard; Protein; 316 AA. 98US-0052521. 97US-0842842. 97US-0880855. 98WO-US07584. 11-FEB-1999 (first entry) Paget's disease 30-MAR-1998; 16-APR-1997; 23-JUN-1997; Homo sapiens. WO9846751-A1. 15-APR-1998; 22-0CT-1998. AAW83194; AAW83194

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The present sequence is human osteoprotegerin (OPG) binding protein.

Host cells transfected with vectors containing nucleic acid molecules
encoding OPG binding protein are used to produce recombinant OPG binding
protein are used to produce recombinant OPG binding
protein is used in binding assays to determine
osteoprotegrin (OC) in biological samples; to screen for specific
binding agents (particularly agonists and antagonists, including
intracellular proteins); to raise Ab (useful in immunoassays for
detection of OPG binding protein) and to identify compounds that
modulate binding of OPG binding protein to osteoclast differentiation
and activation receptor (ODAR). The nucleic acid molecule enroding OPG
binding protein can be used to detect OPG binding protein-encoding
sequences, e.g. screening for related sequences, also to produce
transgenic animal models, while complementary sequences are used for
antisense regulation of OPG binding protein expression. Modulators of
OPG binding protein, particularly soluble forms of OPG binding protein
or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
disease, periodontal disease, osteoporosis, loosening of prostheses,
coptionally in combination with agents that promote bone growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGGG 60
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100.0%; Pred. No. 2.2e-143;
Live 0; Mismatches 0;
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                                                                                 Claim 19; Fig 1; 47pp; English,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 316; Conservative
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                    e.g. treating bone and for diagnosis
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(OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma calls cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (soBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents an osteoclastogenesis inhibitory factor
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for, e.g. treatment and investigation of disorders of bone and
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Tsuda E:
                                                                                                                                                                                                                                        Kobayashi F,
Tomoyasu A,
Yasuda H;
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                                                                                                                                                                                                         (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                        Goto M, Higashio K, Kinosaki M, F
Nakagawa N, Shima N, Takahashi K,
Washida N, Yamaguchi K, Yano K, 1
                                                                                                                                                                       97JP-0224803.
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Best Local Similarity 100.0
Matches 316; Conservative
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calcium metabolism
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09-JUN-1997;
12-AUG-1997;
21-AUG-1997;
W09846644-A1
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VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240

181

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in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation (e.g. cancerous conditions) or degenerative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the method of the invention to treat conditions associated with abnormal physiology or development. The 495B9 protein is expressed highly on polarised ThI T cells, binding of 495B9 protein is expressed result in either immune cell expansion or apoptosis. Antagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus. Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development
                                                                                                                                                             Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis; antagonist; autoimmune disorder; rheumatoid arthritis; systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis; acute inflammatory response; antibody; antigen; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the mouse 499E9 protein, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1675; DB 19;
100.0%; Pred. No. 2.2e-143;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           /note= "intracellular domain"
70..316
/note= "extracellular domain"
                                                                                                                             Amino acid sequence of mouse 499E9 protein.
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                 AAW59654 standard; Protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Pages 8-11; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0032846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US22766
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman DM, Mattson JD;
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N-PSDB; AAV41489.
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                                                                                       24-SEP-1998
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                                                   AAW59654;
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AAW59654
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The present sequence represents murine TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fargments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisens sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing tell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cannoter, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially
TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen.
                                          VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF like proteins for treating autoimmunity and cancer
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                                                                                                                                                                                                       AAY17874 standard; Protein; 316 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 3; 164pp; English.
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                                                                                                                   DQDATYFGAFKVQDID 316
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N-PSDB; AAX80224.
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                                                                                                                                                                                                                                                                                               Murine TRANCE.
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12-DEC-1997;
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Sequence

61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120

1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGCQ 60

Best Local Similarity 100. Matches 316; Conservative

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Query Match

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Gaps

Length 316; Indels 4

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                                                                                                                                                              300
                                                                                                                      240
                                                                                                                                                                                                                                                                                       VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH; parathyroid hormone.
                                                                               1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapapasrsmflallglglgg
                                                                                                                                                                                                                                                                         VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP
                                                       MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGO
                                                                                                                                                                                                                     VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
                          ;
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 Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; osteoclastogenesis inhibitory factor binding molecule;
                            Indels
Score 1675; DB 20;
Pred. No. 2.2e-143;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse OBM protein sequence SEQ ID NO:10
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100.0%;
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Query Match 100.
Best Local Similarity 100.
Matches 316; Conservative
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has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor such as active type vitamin D3 and parathyroid hormone (PTH). The protein can be used as a drug and a research reagent. The present sequence represents a mouse OCIF binding molecule (OBM) from the present
                                                                                                                                                                                                                                                                                                                                                                         121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
                                                                                                                                                                                                                                                                                                                        181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY 240
                                                                                                                                                                                                                                                                                                                                                                                                                          61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                Osteoprotegerin ligand, OPGL, osteoprotegerin, osteoclastogenesis, tumour necrosis factor receptor; type II transmembrane protein, osteoclast differentiation; CSF-1; osteoclast activator;
                                                                                                                                                                                                   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPAASRSMFLALLGLGLGO
                                                                                                                                                                                                                                                                                                                                                                                                              VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP
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                                                                                                                                               Length 316;
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te= "tumour necrosis factor-like domain"
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                                                                                                                                               DB 21;
                                                                                                                                             100.0%; Score 1675; DB 21; 100.0%; Pred. No. 2.2e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response; osteoporosis; bone resorption.
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158..317
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                                                                                                                                                           Best Local Similarity
Matches 316; Conser
                                                                                                          316 AA;
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                                                                                 nvention.
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                                                                                                         Sequence
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                                                                                                                                               Query Match
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The present sequence represents a murine ostcoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumnour necrosis factor. Costeoprotegerin is a secreted member of the tumnour necrosis factor. The operation of the tumnour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The of CSF-1. OPGL is also an activator of mature osteoclasts. The oPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                 In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
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                                                                                                                                                                                                                        to treat, prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                             Claim 17; Page 81-82; 110pp; English
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98DK-0001164
98US-0102896
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                                                                                                Haaning J;
                                                                                                                                     WPI; 2000-271444/23.
N-PSDB; AAZ99965.
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15-SEP-1998;
02-OCT-1998;
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The present sequence represents a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-I. It is not capable of inducing osteoclast differentiation in the absence of CSF-I. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
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tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
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                                                                                                                                            /note= "extracellular stalk domain"
158..317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                             immune response; osteoporosis; bone resorption.
                                                                                                                      "transmembrane region"
                                                                                                                                                                                  /note= "active ligand moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 85-86; 110pp; English.
                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         98DK-0001164
98US-0102896
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                                                                                                                                    ..157
                                                                                                                       /note=
70..157
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                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-271444/23.
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Best Local Similarity
Matches 316; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ99966.
                                                                                                                                                                                                                 WO200015807-A1
                                                             Mus musculus
                                                                                                                                                                                                                                                                             13-SEP-1999;
                                                                                                                                                                                                                                                                                                         15-SEP-1998;
02-OCT-1998;
                                                                                                                                                                                                                                               23-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Region
                                                                                                                                       Domain
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VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT -- LPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPAASRSMFLALLGLGLGCQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding rat osteoclast differentiation factor useful for modulating activity of a cell, e.g., cell proliferation, cell differentiation and cell viability -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                               Rat; osteoclast formation inducer; vaccine; gene therapy; Osteoclast Differentiation Factor; bone.
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Pred. No. 2.5e-136;
5; Mismatches 9;
                                                                                                                                                                                                                                     Rat osteoclast differentiation factor, ODF
                                                                                                                                                     AAB82092 standard; Protein; 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYWA-) UNIV WESTERN AUSTRALIA
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95.0%;
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                                                                                                                                                                                                           (first entry)
                                                                      301 DQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-335526/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 AA;
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                                                                                                                                                                                                                                                                                                                                  WO200123549-A1
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                                                                                                                                                                                                           29-JUN-2001
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                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                AAB82092;
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Matches
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response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF·KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t
                                                                                                                                          239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
kqafqgavqrelqhivgpqrfsgvpammegswldvarrgkpeaqpfahltinaadipsgs 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a murine RankL, a ligand for the Rank (receptor activator of necrosis factor-kappaB (NF-kB) polypeptide. Rank is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated Rank with a soluble RANK which binds the RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                          179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF-kB receptor activator RANK ligand (RANKL).
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                                                                                                                                                                                                                                                                                                                                              AAW69956 standard; Protein; 294 AA.
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96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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07-MAR-1997;
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                                                                                                                       PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
                                                                                                                                                                                  203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
                                                                                                              83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
                                                            Gaps
                                                                                      23 GVPHEGPLHPAPSAPAPAPAPASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - useful
                                                                                                                                                                                                                                                                                                                                                    RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
                                                                                                                                                                                                                    263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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                                           Length 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated receptor activator of necrosis factor-kappa for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
                                                            Indels
                                           DB 19;
                                                   1.8e-132
                                                                                                                                                                                                                                                                                                                                  receptor activator RANK ligand (RANKL).
                                                    Pred. No. 1.86
0; Mismatches
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                                           Score 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80pp; English
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                                           92.8%;
99.7%;
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96US-0059978.
97US-0813509.
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                                                            Conservative
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N-PSDB; AAV41371.
                                                   Similarity
                 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Pages
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus,
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                                                            293;
screening
                  Sequence
                                           Query Match
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                                                     Local
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                                                                                                                                                                                                                                                                                                                                   NF-kB
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nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-KB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of the NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products can also be used for detection and drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVPHEGPLHPAPSAPAPAPAPASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 gklrvnqdgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine receptor activator of NF kappaB ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                   Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                   Score 1554; DB 19;
Pred. No. 1.8e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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970S-0064671.
960S-0772330.
970S-0813509.
970S-0996139.
                                                                                                                                                                                                                                                                                                                                                                              92.8%;
ilarity 99.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                         294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6271349-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1996;
07-MAR-1997;
22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2001.
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14-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE08737;
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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AAE04425 standard; Protein; 294

(first entry)

04-SEP-2001

AAE04425;

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New receptor activator of NF-kappaB (RANK) polypeptides, useful for regulating immune response, in screening for RANK inhibitors, or as an adjunct therapy for disease characterized by neoplastic cells that
                                                                                                        Example 15; Column 65-68; 47pp; English.
 Galibert
                               N-PSDB; AAD15310
                                                                                   express RANK
 Dougall WC,
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and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are useful for the expression of recombinant proteins, as probes for analysis of the presence or distribution of RANK transcripts, while the proteins are useful in preparing kits for the detection of soluble RANK, or monitor RANK related activity. The present sequence is RANK ligand (RANKL) protein from murine.

294 AA; Sequence

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                                                                                                                 202
                                                                                                    DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
                          Gaps
                                                                1 gyphegplhpapsapapappaasrsmflallglglggyvcsialflyfraqmdpnrise 60
                                                23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE 82
                                                                                                                                                                                                                       PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                                                                                                                                                       GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                           263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                        ;
92.8%; Score 1554; DB 22; Length 294; 99.7%; Pred. No. 1.8e-132;
                         Indels
                         Mismatches
                         Conservative
             Similarity
           Local Sim
 Query Match
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RESULT

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                                                                                              Murine, receptor activator of NF-chi B; RANK; tumour necrosis factor; CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF; chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA molecules, useful for producing ligands (which are useful for regulating immune response and in screening for inhibitors of NF-chi B receptor activator) of the receptor activator of NF-chi B (RANK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to receptor activator of NF-chi B (RANKL) DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane proteins respectively. RANK is a member of the tumour necrosis factor (TNF) superfamily and it closely resembles CD40 in the extracellular region. RANK associates with TNF receptor-associated factor (TRAF) 2 and TRAF3. The DNA molecules are useful for reducing ligands of RANK. The ligands are useful for regulating immune response and in screening for inhibitors of RANK. The present sequence is murine RANKL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKLRVNQDGFYYLXANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gvphegplhpapsapapapppaasrsmflallglglggvvcsialflyfragmdpnrise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 GVPHEGPLHPAPSAPAPAPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 294;
                                                                Murine receptor activator of NF-chi B ligand (RANKL) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.8%; Score 1554; DB 22;
99.7%; Pred. No. 1.8e-132;
live 0; Mismatches 1;
                                                                                                                                                                                                                                     /note="Receptor binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Column 59-62; 43pp; English.
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           97US-0077181.
97US-0064671.
                                                                                                                                                                                                                                                                                                                                         97US-0995659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.83
Best Local Similarity 99.73
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-407216/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD08714.
                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                       US6242213-B1.
                                                                                                                                                                                                                                                                                                                                         22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson DM;
                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-1997;
                                                                                                                                                                                                                                                                                                        05-JUN-2001
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                                                                                                                                                                                                                      Region
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The present invention relates to a novel receptor, referred to as RANK (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (receptor activator of NF (nuclear factor)-kappaB), a member of TNF (tumour necrosis factor) receptor superfamily. RANK is a Type I transmembrane protein that interacts with TNF receptor-associated factors (TRAFS). Triggering of RANK by overexpression or co-expression of RANK and membrane bound RANK ligand (RANK) results in upregulation of the transcription factor NF-kappaB, a ubiquitous transcription factor that is most extensively utilised in cells of the immune system.

Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating negative effects of inflammatory reactions, and the effects of excess bone resorption. The RANK DNAs, proteins and their analogues are useful for the preparation of pharmaceutical compositions, for infecting target for the preparation of pharmaceutical compositions, for infecting target associated with RANK, and as targets for use in screening assays. They may be used in the treatment or diagnosis of immune system dysfunction. The present invention also encompasses gene therapy methods to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein; TNF receptor-associated factor; TRAF; TRANK ligand; RANKL; osteopathic; inflammatory reaction; bone resorption; gene therapy; immunomodulator; immune system dysfunction; familial expansile osteolysis; FEO;
240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding a receptor activator of NF-kappaB polypeptide for thereatment of Paget's disease and Familial Expansile Osteolysis (FEO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene-activating mutations, associated with e.g. familial expansile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteolysis (FEO) and early onset Paget's disease of bone (EP). The present amino acid sequence is murine RANKL (muRANKL) protein.
181 gklrvngdgfyylyanicfrhhetsgsvptdylqlmvyvvktsikipsshnlmkggstkn
                                                                                   WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
                                                                                                                                Murine RANKL (receptor activator of NF-kappaB ligand) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           early onset Paget's disease of bone; EP; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 74-75; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       AAE01992 standard; Protein; 294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-2000; 2000WO-US31459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0442029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson DM, Hughes AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-329222/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136637-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE01992;
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                                                                                   263
                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                           AAE01992
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The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; Paget's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                            202
                                                                                                                                                                                                      142
                                                                                                                                         262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding osteoprotegrin binding protein - useful for, e.g. treating bone diseases by modulating osteoclast differentiation
              23 GVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                            83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA
                                                                                                                         143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                                                                                                                                      203 GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences, e.g. screening for related sequences, also to produce
                                                                                                                                                                                                                                                   263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                   ξ
                                                                                                                                                                                                                                                                                                                                                                Protein; 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Fig 4; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                             AAW83195 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. treating bone
and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV70285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9846751-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1999
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23-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                           AAW83195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boyle WJ;
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                                                                                                                                                                                                                                                                                                                                                AAW83195
                                                                                                                                                                                                                                                                                                                                  RESULT
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Gaps

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Length 294; Indels

Score 1554; DB 22; Pred. No. 1.8e-132; 0; Mismatches 1;

92.8%; 99.7%;

Query Match 92.8 Best Local Similarity 99.7 Matches 293; Conservative

us-09-671-658a-2.rag

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antisense regulation of OPG binding protein expression. Modulators of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                        298
                                                                                                                                                                                                                                                           VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                      9
                                                                                                                                                                                                                                 1 mrrasrdytkylrgseemgggpgaphegplh-appppaphgppaasrsmfvallglglgg 59
                                                                                                                                                                                                      1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGQ
                                                                                                                                                                                                                                                                                                               KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS
                                                                                                                                                                                                                                                                                                                                                                   HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                                 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                      human;
                                                                                                                                                 DB 19; Length 317;
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RANK; necrosis factor-kappa B; NF-kB; receptor activator; hu immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                            31; Indels
                                                                                                                                              84.6%; Score 1417.5; DB 1'84.3%; Pred. No. 4.4e-120; ive 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW69957 standard; Protein; 317 AA.
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96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                              Best_Local Similarity 84.3
Matches 268; Conservative
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N-PSDB, AAV41378.
                                                                                                        317 AA;
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07-MAR-1997;
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This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK member of the tumour necrosis factor (TNF) family. A soluble RANK which binds to expressing membrane-associated RANK with a soluble RANK which binds to expressing membrane-associated RANK with a soluble RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chancherapy or the presence of high levels of the products can also be used for detection and drug drug
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inhibiting an
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New isolated ligand for receptor activator of NF-kappa develop products for augmenting an immune response for inflammatory response and for protection of cells
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; Pred. No. 4.4e-120;
16; Mismatches 31;
                                                                        Claim 27; Pages 59-60; 80pp; English
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2002, 11:01:30 ; Search time 30.24 Seconds (without alignments) 1807.751 Million cell updates/sec Run on:

US-09-671-658A-2

1675 1 MRRASRDYGKYLRSSEEMGS.....LLDPDQDATYFGAFKVQDID 316 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

562222 segs, 172994929 residues Searched:

562222 al number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

sp_archea:* sp_bacteria:* SPTREMBL_19:* Database

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_virus:*
sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_plant:* sp_rodent:* sp_mammal:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
-	1646.5	98.3		11	O9R1YO	O9r1v0 mus musculu
2	1597	95.3		11	O9ESE2	O9ese2 rattus norv
9	1476.5	88.1	287	11	Q9JJK9	0911k9 mus musculu
4	1220			4	096017	096917 homo sapien
2	1057			11	09ллк8	0911k8 mus musculu
9	272			11	Q91ZI9	091219 rattus norv
7	263.5	15.7		13	Q9DDZ5	09ddz5 brachydanio
80	217.5	13.0		13	Q90WT9	090wt9 gallus gall
6	188.5	11.3		9	Q9BDN3	Ogbdn3 callithrix
10	182.5	10.9		9	О	O9bdm3 actus trivi
11	179.5	10.7		9	Q9BEA8	O9bea8 sus scrofa
12	179.5	10.7		9	Q95M04	O95m04 sus scrofa
13	. 179	10.7		9	Q9BDM5	O9bdm5 macaca mula
14	178.5	10.7		9	Q95N10	095n10 sus scrofa
15	178	10.6		9	Q9MYL6	Q9my16 macaca neme
16	177	10.6		9	09BDN1	Ogbdn1 cercocebus

Score 1646.5; DB 11; Length 313; Pred. No. 4.3e-139;

98.3%; 99.1%;

Query Match Best Local Similarity

Q9bdc7 macaca mula Q918d8 gallus gall Q9bdm7 macaca neme Q9ttj3 equus cabal O35853 mus musculu Q9jm10 marmota mon Q9gyb9 mus musculu Q927b7 rattus norv Q9r224 rattus norv Q9r224 rattus norv Q9r226 rattus norv Q9131 marmota mon Q91310 homo sapien Q9310 homo sapien Q9930 capra hircu Q99nd1 tamiasciluru Q99741 homo sapien Q99721 sapta hircu Q99711 and A000 sapien Q99721 capra hircu	091198 actus vociti 091102 homo sapien 070312 mesocricetu 09beal tursiops tr 09bec5 tenrec ecau 09beg1 bradypus tr 09beg0 cyclopes di 09x47 macropus eu 09xe9 ochotona pr
Q9BDC7 Q918D8 Q9TBD8 Q9TBD7 Q9TBD3 Q9TBD10 Q9JM10 Q9ZV2 Q9GZV2 Q9GZV2 Q9GZV2 Q9GZV2 Q9GZV2 Q9JIV3 Q9JIV3 Q9JIV3 Q99ND1 Q99ND1 Q99ND1 Q99ND1 Q99RG6 Q99FG6 Q99FG6	09758 097768 0961D2 070332 09BEC5 09BEC1 09BEG1 09BEC1 09BEC9
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111 122 133 133 133 133 133 133 133 133	0 K W W A A A A A A A A A A A A A A A A A

ALIGNMENTS

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MEDLINE-99214075; PubMed-10196481;
Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A., Pudaira M., Higashio K., Mizuno A., Yasuda H., Shima N., Murakami A., Cloning and characterization of the gene encoding mouse osteoclast differentiation factor.";
Gene 230:121-127(1999).
EMBL; AB022039; BAA36970.1; -.
EMBL; AB022037; BAA36970.1; JOINED.
EMBL; AB022037; BAA36970.1; JOINED.
EMBL; AB022037; BAA36970.1; JOINED.
EMBL; AB022039; BAA36970.1; JOINED.
                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS50049; TNF_2; 1.
SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;
                                            09R1YO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0STECCLAST DIFFERENTIATION FACTOR.
                                313 AA
                                PRT;
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InterPro; IPR003263; TNF_5.
InterPro; IPR00478; TNF_family.
Pfam; PF00229; TNF; INF_family.
ProDom; PD008600; TNF; 1.
                                PRELIMINARY;
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RESULT
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HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
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EMBL; AB032771; BAA97257.1; -.
HSSP; P50591; ID0G.
MGD; MGI:1100089; Tnfsf11.
InterPro; IPR003263; TnF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_abc.
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ProDom; PD002012; TNF_abc; 1.
ProDom; PD0006600; TNF_5; 1.
SMART; SM0207; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 287 AA; 33234 MW; 8
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Mammalia; Eutheria; Rodentia;
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                                                                                                             DPDQDATYFGAFKVQDID 316
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tes 285; Conserv
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RA Zheng M.H.;

R. Cloning, sequence and functional characterization of the rat r. Cloning, sequence and functional characterization of the rat r. Domologue of receptor activator of NP-kB ligand.";

R. J. Bone Miner. Res. 15:2178-2186(2000).

RE J. BRBL, AR187319, AAG17031.1;

BRBL, AR187319, AAG17031.1;

InterPro; IPR003263; TNF_5.

InterPro; IPR003263; TNF_5.

InterPro; IPR000600; TNF_1.

DR Pfam; PP008600; TNF; 1.

DR Pfam; PP008600; TNF; 1.
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Sciurognathi; Muridae; Murinae; Rattus.
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                        MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRSMFLALLGLGLGQ
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318 AA; 35370 MW; 4B87A4D706AD098F CRC64;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
NCBI_TaxID-10116,
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95.0%;
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Matches 302; Conservative
Conservative
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PROSITE; PS50049; TNF_
SEQUENCE 318 AA; 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-21150053; Pubmed-11250921;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of Three Isoforms of the Receptor Activator of Nucle Factor-kappaB Ligand and Their Differential Expression in Bone and
241 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISVQVSNPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.1%; Score 1476.5; DB 11; 90.2%; Pred. No. 6e-124; Live 1; Mismatches 1; In
                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
LIGAND 2.
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HSSP; P50591; 1D0G.
MGD; MGI:1100089; Tnfsf11.
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TNFSF11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                   109 DT -- LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAH 166
                                                                                                                                                                                                                                                                                                                                        49 MFLALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESE 108
                                                                                                                                                                                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                                                                                                   227 SGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGE
                                                                                                                                                                                                                                                                                                                                                                                                                               LIINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHET
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Sukaryota: Metazoa, Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae: Mus
                                                                                                                                                                                                                                                                                             Query Match 72.8%; Score 1220; DB 4; Length 270; Best Local Similarity 84.8%; Pred. No. 4.7e-101; Matches 229; Conservative 16; Mismatches 23; Indels
                                                                                                                                                                                                   SEQUENCE FROM N.A.

Ikeda T., Kuroyama H., Hirokawa K.;

Human RANKI isoform."

Submitted (AWT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AB061227; BAB71768.1; -.

SEQUENCE 270 AA; 30522 MW; 5C7754CE32E6F368 CRC64;
                                                                                                 Created)
Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR ACTIVATOR OF NF-KB LIGAND 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09JJK8;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thymus.";
Endocrinology 142:1419-1426(2001).
EMBL; AB032772; BAA97258.1;
                                                                                               01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, HRANKL 2.
           272 DQDATYFGAFKVQDID 287
                                                                            PRELIMINARY;
DQDATYFGAFKVQDID
                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                NCBI_TaxID=9606;
                                                                           096017
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301
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Odgren P.R., Kim N., van Wesenbeeck L., MacKay C.A., Mason-Savas A., Safadi F.F., Popoff S.N., Lengner C., van Hul W., Choi Y., Marks S.C.; "Evidence that the rat osteopetrotic mutation toothless (11) is not in "Evidence that the rat osteopetrotic mutation toothless (11) is not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                       118 MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                            Length 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 SGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF425669; AAL23963.1; -.
InterPro; IPR003263; TNF_5.
InterPro; IPR003263; TNF_6.
InterPro; IPR003636; TNF_family.
InterPro; IPR00478; TNF_family.
ProDom; PD002012; TNF_1.
ProDom; PD008600; TNF_5; 1.
SMART; SM0207; TNF_5; 1.
PROSITE; PS5049; TNF_2: 1.
SEQUENCE 199 AA; 22150 MW; 401C13EB5E8CE166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         63.1%; Score 1057; DB 11;
100.0%; Pred. No. 1.2e-86;
ive 0; Mismatches 0;
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Pred. No. 2.9e-17;
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96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDPDQDATYFGAFKVQDID 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91219;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 199; Conservative
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Pfam; PF00229; TNF; 1.
Probom; PD008600; TNF_5; 1.
SMART; SM0220; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 261 AA; 29360 MW; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P29965; 1ALY.
InterPro; IPR003263; TNF_5.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF344844; AAK37603.1; -
                     13.0%;
26.7%;
                                                                    Conservative
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Best Local Similarity
Matches 77; Conserv
                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 YFGAFRL 285
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                       Query Match
Best Local Simi
Matches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 YANICFRHHETSGSVPTDYLQLMVYVV--KTSIKIPSSHNLMKGGSTKNWSGNSEFHFYS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 RMKQAFQGAVQKELQHIVGPQRFSGAPAMME----GS--WLDVAQRGKPEAQPFAHLTI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                     Bobe J., Goetz F.W.; "Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary"; Comp. Biochem. 129:475-481(2001). EMBL; AF250041; AAG47640.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%; Score 263.5; DB 13; Length 214; 31.5%; Pred. No. 1.1e-15; Live 42; Mismatches 77; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovary.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; %Y057941; AAL23702.1; -.
SEQUENCE 287 AA; 32092 MW; DB06EIC95087B108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98C002474FF691AA CRC64;
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(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 INVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || |:||||:|: ||:|:: ::|||||::: 174 VYQGGLFELRAGDEVFVSVSSPTMVYGEDSSSYFGAFRL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                               HSSP, PSG591; 1D0G.
ZFIN; ZDB-GENE-010801-1; tnfsf101.
InterPro: IPR003263; TNF_abc.
InterPro: IPR0034636; TNF_abc.
InterPro: IPR000478; TNF_family.
Pfam; PF00229; TNF; 1
ProDom; PD0080012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350049; TNF_2; 1.
214 AA; 24093 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50049; TNF.
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                  01-DEC-2001 (TrEMBL)
01-DEC-2001 (TrEMBL)
TRAIL-LIKE PROTEIN.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                            81 SEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFS 140
                                                                                                                                                                                                                                                   141 GAPAMMEGSWLDVAQ---RGKPEAQPFAHLTI---NAASIPSG-----SHKVTLSSW 186
                                                                                                                                                                                                                                                                                         EA----QKSYFNISEGQVATKTLGKPSAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRW 160
                                                                                                                                                                                                                                                                                                                                                                         187 YHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYV-VKTS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 IKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDAT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 YSQPIL--LLKGVGTKCWAPEAERGLHALYQGGLFELKAGDELFVSVSSLAIDYSDAAAS 278
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                                                                                                                                                                                      51 SSEELRCLOLINQQQEGSNLEE--LISN----QSCLKLANTIKAYVATVTENVISRSVVN 104
                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-11gand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
                                                                27;
Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 261;
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SEQUENCE FROW N.A.
MEDLINE-21383618; PubMed-11491535;
Willinger F., Boszlik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
Weiss W.R., Ansari A.A.;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDI54 PROTEIN.
      DB 13;
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                                                                51; Mismatches 103;
Score 217.5; DB 1:
Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                       NCBI_TaxID=9823;
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01-DEC-2001
01-DEC-2001
FAS-LIGAND.
FASL.
                                                                           Sus scrofa
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                                                                                                                                                                                                                                      32 PAPSAPAPAPAPASRSWFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aotus trivingatus (Night monkey) (Douroucouli).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=9505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINGE-21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Welss W.R., Ansari A.A.;
Welss W.R., Ansari A.A.;
Welss W.R., and homology analysis of nonhuman prin
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; Pred. No. 2.5e-08;
49; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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25.8%;
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Q9BEA8;
01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17,
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Best Local Similarity 25.89
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Q9BDM3
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Q9BEA8
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SEQUENCE FROM N.A.
TSUVUKI S., KONO M., Bloom E.T.;
TSUVUKI S., KONO M., Bloom E.T.;
"Cloning and potential utility of porcine Fas ligand: overexpression in porcine cells protects them from attack by human cytolytic cells.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027297; BAB40919.1;
EMBL; AF397407; AAK84408.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-----PLSHKVYTRNSRYPQDLVLME-GKMMNYCTTGQMWARSSYLGAVFNLTSADHL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT 110
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                                                                                                                                                                                                                                            porcine Fas
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                                                       Euteleostomi;
Sus.
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                                                                                                                                 (1)
SEQUENCE FROM N.A.
MEDLINE-21322533; PubMed=11429161;
Muneta Y., Shimoji Y., Inumaru S., Mori Y.;
Molecular cloning, characterization, and expression of ;
ligand (LOD9 119and).";
J. Interferon Cytokine Res. 21:305-312(2001).
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                                                    Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%; Score 179.5; DB 6; Best Local Similarity 21.6%; Pred. No. 5.1e-08; Matches 70; Conservative 42; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01375; 4TSV.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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PRODOM; PD002012; TNF_abc; 1.
PRODOM; PD008600; TNF_5; 1.
PROSTIE; SM0207; TNF, 1.
PROSTIE; PS50049; TNF_1; 1.
PROSTIE; PS50049; TNF_2; 1.
SEQUENCE 282 AA; 31756 MW; 6
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(TrEMBLrel. 19, I
FAS-LIGAND (FAS LIGAND).
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us-09-671-658a-2.rspt

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ProDom; PD002012; TNF_abc; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF_1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS0049; TNF_2; 1.
SEQUENCE 280 AA; 31377 MW; 7
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                                                                                                                                                                                                                             1 Similarity 21.37 67; Conservative
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Best Local Similarity 21.65
Matches 70; Conservative
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Best Local S:
Matches 67,
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                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                            Euteleostomi;
Sus.
                                                                                                                                                   STRAIN-BREED LANDRACE X LARGE YORKSHIRE WHITE (LW); TISSUE-LIVER; Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.; "Genomic Sequence Analysis of Pig Fas-Ligand Gene."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB069764; BAB64291.1; -. SEQUENCE 282 AA; 31722 MW; E54774EBF455127B CRC64;
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MEDLINE-21383618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
"Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
Immunogenetics 53:315-328(2001).
EMBL; AF344856; AAK37539.1; -.
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 179.5; DB 6; Length 282; 21.6%; Pred. No. 5.1e-08; ative 42; Mismatches 105; Indels 107;
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JDEC-2001 (TIEMBLrel. 19, Last annotation update)
FAS ANTIGEN CD95.
Macaca mulatta (Rhesus macaque).
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InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PFO0229; TNF; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01234; TNECROSISFCT.
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                         SEQUENCE FROM N.A
                                                                            NCBI_TaxID=9823;
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Best Local Simi
Matches 70;
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                                                                                                                                                                                                                                                                                60 QVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 MVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 LPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT-- 168
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Zhu N., Young Y.;

"Molecular cloning and characterization of porcine Fas ligand cDNA.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY033634; AAK56449.1; -.

SEQUENCE 282 AA; 31752 MW; F391212406AE1E7D CRC64;
                                                                                                                                                                                                        Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHKVYMRNSKYPQDLVMME-GKMMSYCTTGOMWAHSSYLGAVFNLTSADHLYVNVSELSL
                                                                                                                                                                           22 PGVPHEGPLHPAPSAPAPAPAPASRSM---------FLALLGLGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ----SSLEKQIGHPSPPPE-------KKEQRKVAHLTGKPNSRSMP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 SVPGRP--GQRRPPPPPPPPPPPLLPSRPLPPLPPPSLKKKRDHNAGLCLLVMFFMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 QAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT -- INAASIPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 LALLGLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 282;
                                                                            Length 280;
                                                                       10.7%; Score 179; DB 6; Length 28
21.3%; Pred. No. 5.6e-08;
ive 43; Mismatches 107; Indels
729EA61436F2D398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 178.5; DB 6; 21.6%; Pred. No. 6.3e-08; ive 42; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 AA
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                                                                                                        206 Q-----PLSHKVYTRNSRYPQDLVLME-GKMMNYCTTGQMWARSSYLGAVFNLTSADHL 258
   --KKELRKVAHLTGK 153
                                                                   169 INAASIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAS LIGAND.
PT-FASL OR CM-FASL OR RM-FASL.
Macaca nemestrina (Pig-tailed macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
                                                                                                                                                                                               229 SVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPPPPPPPPPPPPPPPPPPPPPFKKKGNHSTGLCLLVMFFMVLVALVGLGLG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES-M.fascicularis; STRAIN-CYNOMOLGUS MONKEY;
Kirii Y., Inoue T., Yoshino K.;
"Cynomolgus monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
Kirii Y., Inoue T., Yoshino K.;
"Rhesus monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035140; BAA90296.1; -.
EMBL; AB035139; BAA90294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-M.nemestrina; STRAIN-PIG-TAILED MONKEY;
Kiril Y., Inoue T., Yoshino K.;
"Pig-tailed monkey Fas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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31367 MW; F0B284D61A132EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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--ESSLEKQIGHPNLPSE--
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InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_abc.
Pram; PF00229; TNF; IP.
ProDom; PD002012; TNF_abc; IP.
ProDom; PD00800; TNF_5; I.
ProDom; PD00800; TNF_1; I.
PROSITE; PS00251; TNF_1; I.
                                                                                                                                                                                                                                                                                                                               289 SIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                        259 YVNVSELSLVNFEESKTFFGLYKL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Macaca.
NCBI_TaxID=9545, 9541, 9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
Matches 68; Conserva
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SSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVK 243
                                                                                                                                                                          159 LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCTN-----LPLSHKVYM 212
                                                                                                                                                                                                                                                      213 RNSKYPQDLVMME-GKMMSYCTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEES 271
66 ALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFGGA 125
                                                                          126 VQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPSGSHKVTL 183
                                                                                                                                                                                                                                  244 TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQD 303
                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: July 15, 2002, 11:05:29 Job time: 239 sec
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272 QTFFGLYKL 280
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 15, 2002, 11:01:05; Search time 17.53 Seconds (without alignments) 1732.129 Million cell updates/sec

US-09-671-658A-2 1675 1 MRRASRDYGKYLRSSEEMGS......LLDPDQDATYFGAFKVQDID 316 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues Searched:

l number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

283138

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	CD40 liqand - bovi	fas ligand - rat	Fas ligand - mouse		0 lígand -	CD40 ligand - mous	tumor necrosis fac	lymphotoxin-beta -	lymphotoxin beta -	tumor necrosis fac	hypothetical prote		hypothetical prote	P	hypothetical prote	E	collagen alpha 1(I	lymphotoxin alpha											
	ID	S53090	A49266	A53062	138707	153476	S21738	JQ1344	OMMSN	S22052	JH0529	S11688	OWHUN	A25451	154490	S24642	S52715	S12606	JU0029	149139	A46066 .	S06192	S49742	T17414	T23649	149681	S38114	B55514	B40333	омних
	DB	2	7	7	~	7	7	-	-	Н	-	7	-	-	7	Н	~	Н	7	7	7	~	N	7	~	~	7	~	П	
	Length	261	278	279	281	261	260	234	235	233	234	233	233	234	235	233	185	232	235	306	244	193	340	4	558	440	450	553	1486	205
фP	Query Match	11.1	10.9	10.9	10.4	10.2	9.4	8.9	8.7	8.6	8.4	8.4	8.3	8.2	8.1	8.0	7.9	7.9	7.7	7.7	7.0	6.9	6.2		5.9		5.8	•	2.6	2.0
	Score	185.5	183	œ	173.5	171.5	157	4	9	143.5	141	140	139.5	137.5	35	133.5	133	133	129.5	129.5	117	115.5	103.5	103	99.5	66		95.5	94	93.5
	Result No.	1	7	m	4	2	9	7	œ	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	53

tumor necrosis fac secreted klotho pr	hypothetical prote membrane klotho pr	serine/threonine-s probable Athila re	probable insectici	genome polyprotein	sialoadhesin - mou	tumor necrosis fac	adenylyl cyclase-a	hypothetical 176K	hypothetical prote	probable 60K inner	probable cytoskele	microtubule-associ
JH0309	T23456 JC5925	T39500 E84475	AC0447	S40770	S50065	B27303	I38409	JQ0096	H75253	JQ1221	T37781	A43359
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197	1012	658 750	952	3011	1694	202	477	1547	347	260	1420	2774
5.5.5 5.5		5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3
92.5	6 6 6	90.5 90.5	90.5	06	83	88.5	88.5	88.5	88	88	88	88
30	337	35 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT S53090 CCD40 liga CC 5 Species C; Species C; Accessing A; Descrip A; Referen A; Referen A; Referen A; Referen A; Residue A; CLOSS - r. Best Lo Matches Qy 32 Ob 58 Ob 105	RESULT 1 S53090 CiD40 ligand - bovine C;Species: Bos primigenius taurus (cattle) C;Accession: S53090 C;Accession: S53090 C;Accession: S53090 A;Mortens, B.E.L.C.; Muriuki, M. Submitted to the EMBL Data Library, February 1995 A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB. A;Reference number: S53090 A;Accession: S53090 A;Accession: S53090 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-261 <amre> A;Residues: 1-261 <amre> A;Cross-references: EMBL: Z48469; NID: 9732569; FIDN: CAA88363.1; PID: 9732570</amre></amre>	Ouery Match Best Local Similarity 25.1%; Pred. No. 5.4e-08; Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15; 32 PAPSAPAPAPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 90	ILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF	140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN 197 105 KKKEKNFEMHKGDQEPQIAAHVISEASSKTTSVLQWAPKGYYTLSNNL 152	MTLSNGK-LRVNQDGFYXLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN 253	254 LAKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEELSIQVSNPSLLDPDQDATYFGAFKY 312
	REGULT 1 S53090 C1500 ligand C;Species: B C;Date: 08-1 C;Accession: R;Mertens, B submitted to A;Descriptio A;Reference A;Reference A;Accession: A;Ac	Query Ma Best Loc Matches	о и		198	

RESULT A49266

fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Decies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
R;Suda, T; Takahashi, T; Golstein, P; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu A;Reference number: A49266; MUID:94084792

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125 ----SSLEKQIGHPSPPPE-------KKELRKVAHLTGKSNSRSMP- 159
                                                                                                      | | | : : : | : | : | : | SLINFEESKTFFGLYKL 279
                                                                                SLLDPDQDATYFGAFKV 312
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Best Local Similarity
Matches 67; Conservat
                                                                                                                                                                                                 Fas ligand - human
               236
                                                208
                                                                                                                 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Reference number: A53062; MUID:94185175
                                                                                                                                                                 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
                                                                                                                                                                                                                                                                                                                                                       --LSHKVYM--RNFKYPGDLVLME-EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 GMGLG------MYQLFHLQKELAELREFTNH------SLRVSSFEKQIANPST 133
                                                                                                                                                                                                                                                                                                                                115 CRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DYLOLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIOV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KKEPRSVAHLTGNPHSRSIP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 GLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 SSEEMGSG----PGVPHEGPLHPAPSAPAPAPP--------PAASRSMFLALL 54
                                                                                                                                                                                                                                34 SSGPRGPGORRPPPPPPPPPPPPPPPPPPPPPPPPPPPPFKKKDNIELWLPVIFFMVLVALV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSSEEMGSGPGVPHEGPLHPAPSAPAPAPAP-------PAASRSMFLALLGLG 57
                              A; Molecule type: mRNA
A; Residues: 1-278 <SUD>
A; Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565
                                                                                                                                                                                                                                                                                                                                                                                                  SIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT
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                                                                                                                                Length 278;
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                                                                                                                              Score 183; DB 2; Length 27; Pred. No. 9.5e-08; 42; Mismatches 107; Indels
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1.2e-07;
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Pred. No. 1.
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SQLSLINFEESKTFFGLYKL 278
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22.7%;
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                                                                                                                              Query Match
Best Local Similarity
Matches 75; Conserv
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               Status: preliminary
A; Accession: A49266
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Best Local Simi
Matches 72;
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: 138707; JC2340; S57565; I38554
Ent. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas Isgand: gene structure, chromosomal location and species specifici A;Accession: I38707; MUID:95127560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990 R;Schatzlein, C.E. submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross references: EMBL:U1821; NID:9595430; PIDN:AAC50124.1; PID:9595431
B;Mita. E:; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Blochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Recession: JC2340; MUID:95071350
A;Accession: JC2340
A;Accession: JC2340
A;Residues: 1-281 <MIT>
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                                  59 GQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRM 118
QLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNP 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: FasL
A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;80-102/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 PGVPHEGPLHPAPSAPAPAPPPAASR-----
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GenCore version 4.5
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OM protein - protein search, using sw model

July 15, 2002, 11:01:55; search time 13.43 Seconds (without alignments) 911.048 Million cell updates/sec Run on:

US-09-671-658A-2 1675 1 MRRASRDYGKYLRSSEEMGS......LLDPDQDATYFGAFKVQDID 316 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapèxt 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 ll number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

W	Description	5235 m	014788 h tumor nec	homo	mus m	P51749 bos taurus	ratt	P41047 mus musculu	рошо	рошо	felis	cavia	mus mu	097626 canis famil	P29553 equus cabal	P79337 macaca fasc	P48094 macaca mula				ovis a	P19101 felis silve	canis		324 oryct	939 perom	227	599 bos t	P23563 sus scrofa	7	59	11	74	006643 homo sapien
SUMMARIES	ΩI	TN11_MOUSE	TN11_HUMAN	TN10_HUMAN	TN10_MOUSE	TNF5_BOVIN	FASL_RAT	FASL_MOUSE	FASL_HUMAN	TNF5_HUMAN	TNF5_FELCA	TNFA_CAVPO	TNF5_MOUSE	TNF5_CANFA	TNFA_HORSE	TNFA_MACFA	TNFA_MACMU		TNFA_PAPHU	TNFA_PAPSP	TNFA_SHEEP	TNFA_FELCA	TNFA_CANFA	TNFA_HUMAN	TNFA_RABIT	TNFA_PERLE		TNFA_BOVIN	TNFA_PIG	TNFA_MARMO	TNFA_RAT	TNFC_MOUSE	TNFA_CEREL	TNFC_HUMAN
	DB	7	-	П	П	П	П	Н	П	Н	٦	-	7	П	-	П	П	П	П	П	1	Н	Н	П	П	П	Н	H	-	Н	Н		-	Н
	Length	316	317	281	291	261	278	279	281	261	260	234	260	260	234	233	233	235	233	233	234	233	233	233	235	235	240	233	232	233	235	306	229	244
dР	Query	00	84.6	'n.	4	11.1	。	。	0				•	9.5	•		8.8	8.7	•	٠	8.4	٠		٠		٠	•	٠	•			7.7	7.6	7.0
	Score	1675	1417.5	258.5	244	185.5	183	182	173.5	7	164	157	157	154	149	148.5	4	146.5	143.5	143.5	141	140	139.5	139.5	137	135.5	134.5	133.5	133	$^{\circ}$	129.5	29.5	128	117
	Result No.		7	m	4	ស	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P13296 capra hircu	077764 macropus eu	Q9xt48 macropus eu	Q03703 saccharomyc	Q64467 mus musculu	P36135 saccharomyc	Q59098 alcaligenes	P01374 homo sapien	P10154 oryctolagus	Q9ubp0 homo sapien	P50527 schizosacch	Q62230 mus musculu
TNFA_CAPHI	TNFA_MACEU	TNFB_MACEU	YMD7_YEAST	G3PT_MOUSE	YK22_YEAST	ODP2_ALCEU	TNFB_HUMAN	TNFB_RABIT	SPAS_HUMAN	PAK1_SCHPO	SN_MOUSE
П		Н	Н	7	-	-	Н	H	Н	~	7
193	233	201	340	440	450	553	202	197	616	658	1694
6.9	6.5	6.5	6.2	5.9	5.8	5.7	2.6	5.5	5.4	5.4	5.3
115.5	109:5	109	103.5	66	97	95.5	93.5	92,5	91	90.5	83
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

		STANDARD;	RD; Created) Last seq	D; PRT; 316 AA. Created) Last sequence update)	316 updat	AA .	
	1b-OCT-2001 (Rel. 40, Last annotation update) Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor)	factor factor or kap e) (TR	Last ar ligand pa B lic ANCE) ((notatic superfa fand) (F steopro	on upd umily vankl) oteger	ate) member 11 (F (TNF-relate in ligand) (Receptor activator of activation of activation (Obgil) (Osteoclast objitory factor)
	(OCIF). INFSF11 OR RANKL OR TRANCE OR OPGL.	L OR T	RANCE OF	OPGL.		•	
	Mus musculus (Mouse) Eukaryota, Metazoa, Mammalia, Eutheria, NCBI_TaxID=10090;	louse). Izoa; C rria; R	Chordata; Rodentia;	Crania	ıta; V ognath	ertebrata; E i; Muridae;	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
	LIJ SEQUENCE FROM N.A.	. A.					-
		ia; 2; Pub	Med=9312	132;			,
	· 6	J., Ar Cayani	ron J., E., Baı	Robinscribett F	n E., '.S. I	Rho J., Arron J., Robinson E., Orlinick J., S., Cayani E., Bartlett F.S. III, Frankel W	Rho J., Arron J., Robinson E., Orlinick J., Chao M., S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.
~ -	Choi Y.; "mpance is a no	14.	70 Pub.	+ 44+		oroce e	nocrosis feator recentor femily
3 -	that activates J. Biol: Chem.	c-Jun 272:25	is a mover instant of the tumor invates c-Jun N-terminal kinase . Chem. 272:25190-25194(1997).	ual kine 14 (1997)		in T cells.";	in tecepror to
٠,	[2] SECUENCE FROM N.A	, A				,	
	TISSUE=Bone marrow;	row;	2230-804	0			
	Lacey D.L., Timms E., Tan HL., Kelley M.J., Dunstan C.R.,	uns E.,	Tan H.	L., Kel	ley M	.J., Dunstar	C.R.,
	Burgess T., Ell	iott R	., Color	bero A.	, Ell	iott G., Scu	nlly S., Hsu H.
	Kaufman S., Sar	osi I.	Shalh	oub V.,	Senal	5., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney	n., Oelaney J.,
	BOYIE W.J.; "Osteoprotegerin ligand is a cytokine that regulates osteoclast	n liga	nd is a	cytokir	e tha	t regulates	ostèoclast
	differentiation and activation.";	anda	ctivatic	n.";	•	à	
	[3]	(1998)					
	SEQUENCE FROM N.A.	I.A.					
	TISSUE=Bone marrow stroma; MEDLINE=98188248; PubMed=9520411;	row st 8; Pub	roma; Med=952(411;			
	Yasuda H., Shim	la N.,	Nakagawa	N., Yō	ımaguc	Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,	saki M.,
	Mochizuki SI., Tomoyasu A., Yano K., Goto M.,	, Tomo	yasu A.	Yano F	., . 	to M., Murakami	tami A., Tsuda
	Morinaga I., Hi "Osteoclast dif	ferent	iation	actor i	s a l	idand for	inda I.;
	osteoprotegerin/osteoclastogenesis-inhibitory factor and	/osteo	clastoge	nesis-i	nhibi	tory factor	and is identical
	Proc. Natl. Acad.		Sci. U.S.A.	95:35	17-360	95:3597-3602(1998).	_
	[4]						
	SEQUENCE FROM N.A	I.A.					
	11550E-1117HIL 17HPHOMB, MEDLINE=98032977; PubMed=9367155;	7; Pub	a, Med=936]	155;			
Anderson D.M., Maraskovsky E., Billing	Anderson D.M.,	Marask	Maraskovsky E., Billingsley W.L.,	, Billi	ndsle	W.L., Doug	Dougall W.C.

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121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
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                                                                                                                                  JUNEAURITHOUGH (JAN 2000) TO THE EMBL/JOHNA AND GATABASSES.

-1- FUNCTION: OSTEOCLAGT DIFFERENTIATION AND GATIVATION FACTOR.

AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL

PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS

BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE

REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.

-1- SUBCELLIGLAR LOCATION: TYPE II membrane protein (Potential).

-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT

NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN THE

TRABECTICAR BONE AND LUNG.

-1- DISEASE: DEFICIENCY IN THYSFII RESULTS IN FAILURE TO FORM LOBULO-

ALVEOLAR MAMMARY STRUCTURES DURING PREGNARCY, RESULTING IN DEATH

OF NEWBORNS: TRANCE-DEFICIENCY SHOW SEVERE OSTEOPETROSIS, WITH

NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT

PROFOUND GROWTH RETARABATION AT SEVERAL SKELETAL SITES, INCLUDING

THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,

WITH THICK, IRREGULAR GROWH PLATES AND A RELATIVE INCREASE IN

HYPERTROPHIC CHONDROCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                        Ikeda T.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> D (IN REF. 4).
08DF63A2BE00967A CRC64;
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69
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99
316 AA;
                                                                                       SEQUENCE FROM N.A.
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CONFLICT
SEQUENCE
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TW11_HUMAN STANDARD, PRT; 317 AA.
014788 : 014723; O9P203;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
10-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40, Cast annotation update)
116-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40, Cast annotation update)
116-OCT-2001 (Rel. 40, Last annotation update)
116-OCT-2001 (Rel. 40
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                                                                                                                                                                  Galibert L.;
"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                           TISSUE-Lymph node;
MEDLINE-982276G1; PubMed-9568710;
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
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MEDLINE=97460112; bubMed=9312132;
WHOLINE=97460112; bubMed=9312132;
Whong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
VILSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagai M., Kyakumoto S., Sato N.; "Cancer cells responsible for humoral hypercalcemia express mRNA encoding a secreted form of ODF/TRANCE that induces osteoclast formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine that regulates osteoclast
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Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Peripheral blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation factor) (ODF).
TNFSF11 OR RANKL OR TRANCE OR OPGL.
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MEDLINE=20175237; Pubmed=10708588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 73-317 FROM N.A.
                                                                                                                                                                                                                                                                                                                                        301 DQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                                                                                                                                        301 DQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TN11_HUMAN
    181
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Gaps

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100.0%; Score 1675; DB 1; Length 316; 100.0%; Pred. No. 7.4e-131; ive 0; Mismatches 0; Indels 0

Matches 316; Conservative

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Similarity

Query Match Best Local 9

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1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPAASRSMFLALLGLGLGQ

240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLL 299

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chem. Biophys. Res. Commun. 269:532-536(2000).

FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.

AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL

PROLIFERATION. MAY BE AN IMPORTANY REGULATOR OF INTERACTIONS

BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE

REGULATION OF THE T CELL-DEPENDENT IMMONE RESPONSE. MAY ALSO PLAY

AN IMPORTANY ROLE IN BNHANCED BONE-RESORPTION IN HUMORAL

HYPERCALCEMIA OF MALIGNANCY.

SUBCELLLIAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                                          SECRETED (ISOFORM 1).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODE; ARE PRODUCED BY ALTERNATIVE PRODUCES PALICINE.

-!- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART, PLACEMEN, SKELEFAL MUSCLE, STOMACH AND THYROLD.

-!- INDUCTION: UPPRECULATE BY T CELL RECEPTOR STIMULATION.

-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS PACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM 2).
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InterPro; IPR000478; TNF_family.
Pfan; PP00129; TNF; 1.
ProDom; PD0006600; TNF; 1.
PROSITE; SM00207; TNF; 1.
PROSITE; PS50049; TNF_1; PALSE_NEG.
Cytokine; Differentiation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal-anchor; Alternative splicing DOMAIN 1 47 CYTOPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AR037599; BAA90488.1; -. MIM; 602642; -. Intern-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF019047; AAB86811.1; -. EMBL; AF053712; AAC39731.1; -.
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194
317 AA;
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198
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CARBOHYD
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      Biochem.
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                                                                                                                                                                                                               KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                                                 VYVVTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEBISIQVSNPSLL 298
                                                                                                                                           61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT---LPDSCRRM 118
                                                                                                                                                                                                                                                                                  HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
                                      Gaps
                                                                       1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPAASRSMFLALLGLGLGG 60
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(
84.6%; Score 1417.5; DB 1; Length 317; 84.3%; Pred. No. 1.2e-109;
                                    Indels
                                      31;
                                  16; Mismatches
                                    Conservative
                  Similarity
                                  268;
 Query Match
                  Best Local
Matches 26
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766176446348097F CRC64;

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MIM; 603598; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Struct. Biol. 6:1048-1053(1999).
--- FUNCTION: INDUCES APOPTOSIS.
--- SUBUNIT: HOMOTRIMER (POTENTIAL).
--- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
--- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE=96111955; PubMed=8777713; Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2020 (Rel. 41, Last annotation update)
apoptosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
TNFSFIO OR TRAIL OR APO2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
MEDLINE-20017054; PubMed=10549288;
Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in a
complex with death receptor 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I., Jones E.Y., Screaton G.R.; Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation."; Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of a new member of the TNF family that induces apoptosis.";
Immunity 3:673-682(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
                                                                                                                                    281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necrosis factor cytokine family.";
J. Biol. Chem. 271:12687-12690(1996).
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96278649; PubMed=8663110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U37518; AAC50332.1; -. EMBL; U57059; AAB01233.1; -.
299 DPDQDATYFGAFKVQDID 316
                      300 DPDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Cell 4:563-571(1999).
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Placenta;
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                                                                                                                                    TN10_HUMAN P50591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi
                                                                                              RESULT 3
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                     ial-anchor; Apoptosis; 3D-structure.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
DDAAAF78DAAB2F6D CR664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                                                                                                                                                                                                                                                                 101 QDSTLESEDTLPDSCRRMKQAFQGAVQK-------ELQHIVGPQRFSGAPAMM 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                          10 PSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELKQMQDKYSKSGIACF----LKEDDSY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-9611955; Pubmed-8777713;
WILRY S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVQEKQQNISPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein).
                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification and characterization of a new member of the TNF
                                                                                                                                                                                                                                                                               DB 1; Length 281;
                                                                                                                                                                                                                                                                            15.4%; Score 258.5; DB 1; Length 36.4%; Pred. No. 3.3e-14; ive 54; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 AA
PDB; 1D0G; 22-OCT-99.
PDB; 1D4V; 01-NOV-99.
InterPro; 1PR003263; TNE_5.
InterPro; 1PR003636; TNE_abc.
InterPro; 1PR000478; TNF_abc.
Prodom; PD002012; TNF_abc; 1.
Prodom; PD008600; TNF_5; 1.
Prodom; PD008600; TNF_5; 1.
PROSITE; PS00231; TNF; 1.
PROSITE; PS00215; TNF; 1.
PROSITE; PS00215; TNF_1: 1.
PROSITE; PS00219; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                  32509 MW;
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                                                                                                                                                                                                                                281 AA;
                                                                                                                                                                                                                                                                                           Similarity
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-Best Local Similatches 78; C
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                                                                                                                                                                                                                  DOMAIN
SEQUENCE
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TN10_MOUSE
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literPro; interPro; i.

R Pfam; PF00209; TNF; 1.

R ProDom; PD002012; TNF abc; 1.

DR ProDom; PD008000; TNF; 1.

DR SMART; SM00207; TNF; 1.

DR ROSITE; PS00409; TNF_1; 1.

DR PROSITE; PS00409; TNF_1; 1.

DR PROSITE; PS00409; TNF_1; 1.

DR PROSITE; PS00409; TNF_1; 1.

TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

TRANSMEM 18 39 291 EXTRACELLUIAR (POTENTIAL).

TRANSMEM 18 39 291 EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    EMBL outstation
between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 RLHENAGLODSTLESEDTLPDSC----RRMKQAFQGAVQKELQHIVG--PQRFSGAPAMM 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 ---TDEDFWDST--DGEILNRPCLQVKRQLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL---QLMVYVVKTSIKIPS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 SHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ALLGLGLGQ-----VVCSIAL-----FLYFRAQMD--PNRISEDSTHCFYRIL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-000 (Rel. 39, Last annotation update)
CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 HVLFRNGELVIEQEGLYXIYSQTYFRFQEAEDASKMVSKDKVRTKQLVQYIYKYT-SYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 244; DB 1; Length 291; Best Local Similarity 27.5%; Pred. No. 5.3e-13; Matches 83; Conservative 50; Mismatches 111; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA.
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                                                                                                                                                                     MGD; MGI:107414; Tnfsf10.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                 EMBL; U37522; AAC52345.1; -.
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P51749;
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